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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF
SCREENING FOR MODULATORS OF CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 10 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 15 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other 20 diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the 25 American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is 30 in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) *Stem Cells* 16:413-428. Similarly, anti-CD20 monoclonal antibodies
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) *Blood* 90:2188-2195; Leget and Czuczman (1998) *Curr. Opin. Oncol.* 10:548-551.

25 The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a
30 pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting
5 the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is
10 suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as
15 described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological
25 sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and
30 determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for 10 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 15 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous 20 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American 25 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 30 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznek (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwe, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901; 5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the 10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., 15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also 20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin 30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP 5 program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787. 10 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than 15 about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a 20 polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

25 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, 30 www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially 5 identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic 10 acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a 15 silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, 20 adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the 25 invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties 30 Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a 5 polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers 10 to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 15 100 nucleotides in length. Nucleic acids and polynucleotides are polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages 20 (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 25 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of 30 naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

Letsinger (1970) *J. Org. Chem.* 35:3800-3803; Sprinzl, et al. (1977) *Eur. J. Biochem.* 81:579-589; Letsinger, et al. (1986) *Nucl. Acids Res.* 14:3487-499; Sawai, et al. (1984) *Chem. Lett.* 805, Letsinger, et al. (1988) *J. Am. Chem. Soc.* 110:4470-4471; and Pauwels, et al. (1986) *Chemica Scripta* 26:141-149), phosphorothioate (Mag, et al. (1991) *Nucleic Acids Res.* 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) *J. Am. Chem. Soc.* 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) *Oligonucleotides and Analogues: A Practical Approach*, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) *J. Am. Chem. Soc.* 114:1895-1897; Meier, et al. (1992) *Chem. Int. Ed. Engl.* 31:1008-1010; Nielsen (1993) *Nature* 365:566-568; 5
10 Carlsson, et al. (1996) *Nature* 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) *Angew. Chem. Intl. Ed. English* 30:423-426; Letsinger, et al. (1988) *J. Am. Chem. Soc.* 110:4470-4471; Letsinger, et al. (1994) 15
15 *Nucleoside and Nucleotide* 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) *Carbohydrate Modifications in Antisense Research* ACS Symposium Series 580; Mesmaeker, et al. (1994) *Bioorganic and Medicinal Chem. Lett.* 4:395-398; Jeffs, et al. (1994) *J. Biomolecular NMR* 34:17; Horn, et al. (1996) *Tetrahedron Lett.* 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi 20
20 and Cook (eds. 1994) *Carbohydrate Modifications in Antisense Research* ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) *Chem. Soc. Rev.* pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) *C&E News*.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal 25
25 mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively 30
30

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand 5 also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically 10 refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

15 A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, 20 proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly 25 used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound 30 (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, 5 through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

10 As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage 15 other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with 20 isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, 25 protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. 30 By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the 5 in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein 10 is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at 15 least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally 20 seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates 25 that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences 30 that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

- sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.
- An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times
5 background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For
10 high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high
15 stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy
20 permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar
25 stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly
30 or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., 5 fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness 10 into Matrigel, tumor growth and metastasis *in vivo*, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, 15 measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GPP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of cancer polynucleotide and polypeptide sequences. 20 Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. 25 Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for 30

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

- 5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

- 10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these
- 15 light and heavy chains respectively.

- Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to $V_H\text{-}C_H1$ by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

- For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

5 Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

10 A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a 15 variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

20 In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic 25 cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

30 The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression 5 profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be 10 evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are 15 differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other 20 organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

25 Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer 30 sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher
10 being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).
20 Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

25 Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access
30 to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

- 5 The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.
- 10 Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

- Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)
- Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)
- 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.
- 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method 5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount 10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, 15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, 20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes 25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a 30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

- 5 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can
10 be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal
15 comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

- 5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase
- 10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In 15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH 20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain 5 of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For 10 example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 15 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not 20 limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved 25 motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth 30 factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ*. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

5 Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment

10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the

15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,

20 moderate or low stringency conditions may be used; see Ausubel, *supra*, and Tijssen, *supra*.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of

25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent

30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one
5 embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

10 In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and
15 the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary
20 target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and
25 properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either
30 overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or

- 5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

- 20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonJ, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature 5 provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).
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Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained 15 sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in 20 screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, *supra*, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid 25 operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is 30 operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous.

5 Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression

10 vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and

15 stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

20 An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two

25 homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) *Proc. Nat'l Acad. Sci. USA* 92:9146-9150.

30 In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization.

For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeabacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

20 In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes:

5 substitational, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis
10 using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

15 While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR
20 mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

25 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions
30 may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will 5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by 10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's 15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an 20 electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same 25 immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of 30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases.

- 5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

- 10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-
15 terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide
20 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

- Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may 5 reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.)
10 Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the
15 recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized
20 antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
25 immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding
30 sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) *J. Mol. Biol.* 227:381-388; Marks, et al. (1991) *J. Mol. Biol.* 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) *Monoclonal Antibodies and Cancer Therapy* Liss; and Boerner, et al. (1991) *J. Immunol.* 147:86-95).

- 5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S.
10 Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) *Bio/Technology* 10:779-783; Lonberg, et al. (1994) *Nature* 368:856-859; Morrison (1994) *Nature* 368:812-13; Fishwild, et al. (1996) *Nature Biotechnology* 14:845-851; Neuberger (1996) *Nature Biotechnology* 14:826; and Lonberg and Huszar (1995) *Intern. Rev. Immunol.* 13:65-93.

- 15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety. Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

10 The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM , preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding to the specific target and not to related sequences is often also important.

15 Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide 20 expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile 25 of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

30 "Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

10 In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or 15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

15 As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or 20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following 25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

20 In another preferred method, antibodies to the cancer protein find use in *in situ* imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with 30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, *in situ* hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. *In situ* hybridization (see, e.g., Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

25 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or 5 heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" 10 is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, 15 creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive 20 Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify 25 those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical 30 library, such as a polypeptide (e.g., murein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallo, et al. (1994) *J. Med. Chem.* 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) *Pept. Prot. Res.* 37:487-493, Houghton, et al. (1991) *Nature* 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) *J. Amer. Chem. Soc.* 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) *J. Amer. Chem. Soc.* 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) *J. Amer. Chem. Soc.* 116:2661-662), oligocarbamates (Cho, et al. (1993) *Science* 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) *J. Org. Chem.* 59:658). See, generally, Gordon, et al. (1994) *J. Med. Chem.* 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) *Nature Biotechnology* 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) *Science* 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) *C&EN*; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

5 The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of
10 particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody
15 binding.

In addition, high throughput screening systems are commercially available (see, e.g.,
20 Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These
25 configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding,
and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in
30 this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 15 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

20 A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, 25 salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

30 The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another 10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens 15 are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to 20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be 25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of cancer 30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate,
10 e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes
20 are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
25 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a
30 non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, 10 hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For 15 example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For 20 measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., - fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

25 Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

30 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

5 In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

10 In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

15 Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface 25 of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular 30 manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.
25

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

- 5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.
- 10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

- 5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Insti. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

5 Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

10 Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into 25 Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other 30 extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth *in vivo*

Effects of cancer-associated sequences on cell growth can be tested in transgenic or
5 immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the
10 endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the
15 chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) *Science* 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

20 Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) *J. Natl. Cancer Inst.* 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) *Br. J. Cancer* 38:263-272; Selby, et al. (1980) *Br. J. Cancer* 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected
25 into isogenic hosts will produce invasive tumors in a high proportion of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction
30 (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer**Antisense and RNAi Polynucleotides**

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) *Cancer Res.* 48:2659-2668; and van der Krol, et al. (1988) *BioTechniques* 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brummelkamp, et al. (2002) *Scienceexpress* (21 March 2002); Sharp (1999) *Genes Dev.* 13:139-141; and Cathew (2001) *Curr. Op. Cell Biol.* 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general 10 review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

20 Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the 25 ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

30 Thus, in one embodiment, methods of modulating cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene 5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other 10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic 15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one 25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to 30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

5 In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 **Administration of pharmaceutical and vaccine compositions**

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)

15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Rennington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, 5 or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising 10 nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

15 The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, 20 cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

25 In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the 30 genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) *J. Clin. Invest.* 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) *Molec. Immunol.* 28:287-294; Alonso, et al. (1994) *Vaccine* 12:299-306; Jones, et al. (1995) *Vaccine* 13:675-681), peptide compositions contained in 5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) *Nature* 344:873-875; Hu, et al. (1998) *Clin Exp Immunol.* 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) *Proc. Natl. Acad. Sci. USA* 85:5409-5413; Tam (1996) *J. Immunol. Methods* 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 10 379, in Kaufmann (ed. 1996) *Concepts in Vaccine Development* de Gruyter; Chakrabarti, et al. (1986) *Nature* 320:535-537; Hu, et al. (1986) *Nature* 320:537-540; Kieny, et al. (1986) *Bio/Technology* 4:790-795; Top, et al. (1971) *J. Infect. Dis.* 124:148-154; Chanda, et al. (1990) *Virology* 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) *J. Immunol. Methods* 192:25-35; Eldridge, et al. (1993) *Sem. Hematol.* 30:16-24; Falo, et al. 15 (1995) *Nature Med.* 1:649-653), adjuvants (Warren, et al. (1986) *Annu. Rev. Immunol.* 4:369-388; Gupta, et al. (1993) *Vaccine* 11:293-306), liposomes (Reddy, et al. (1992) *J. Immunol.* 148:1585-1589; Rock (1996) *Immunol. Today* 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) *Science* 259:1745-1749; Robinson, et al. (1993) *Vaccine* 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) *Concepts in Vaccine Development* de 20 Gruyter; Cease and Berzofsky (1994) *Annu. Rev. Immunol.* 12:923-989; and Eldridge, et al. (1993) *Sem. Hematol.* 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance 25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, 30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quill A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

- 5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. 10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

- Methods for the use of genes as DNA vaccines are well known, and include placing a 25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a 30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may 5 include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated 10 activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or 15 outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and 20 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangiitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmentary vitonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), sclerite/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma *in situ*, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskeletal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)
brain: glioblastoma, oligodendrogloma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, cranioopharyngioma, pineoblastoma, pheochroma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma *in situ*, lobular carcinoma *in situ*
cervix: cancer of the cervix, vagina, or vulva
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastroduodenal carcinomas
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- 25 head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinoma (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomyolipoma, oncocytoma
- 30 leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangiitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 35 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor like conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoïd, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
- 40 ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrial tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulocystic stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
- pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreaticoblastoma, duodenal-mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
- 45 prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma *in situ*, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular naevi (congenital or acquired neoplasm of melanocytes), acinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), xanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma), tumors of the blood and lymph vessels (e.g., angiomyoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors), granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskelatal Ewing's sarcoma, schwannoma, neuroma, ganglion neuroma, paraganglioma, extraskelatal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotential mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenoacanthoma, carcinoïd, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
- 60 testes: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex cord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and para-testicular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the male testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
- uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenocarcinoma)
- 65

70 Tables 2B-72B, 76B, and 79B list accession numbers for Pkeys lacking Unigene ID's for Tables 2A-72A, 76A, and 79A, respectively. For each probe set is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-72C, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-72A, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probe set identifier number
ExAccn: Exemplar Accession number
UnigeneID: Unigene ID number

	Unigene Title:	Unigene gene title
	Disease:	preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
5	Utility:	preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)
10	Pkey; ExAccn; UnigeneID; Unigene Title; Disease; Utility	
	102892; BE440842; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.	
	104865; T79340; Hs.22575; B-cell CLLymphoma 6, member 1; angio; CTL	
15	104978; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL	
	108424; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.	
	110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag	
	110906; AA035211; Hs.17404; SOX SRY (sex determining reg); angio, blad; CTL	
	115622; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL	
20	116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL	
	118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung, diag	
	123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag	
	131498; FD6972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.	
	133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag	
25	310016; AW449612; Hs.152475; ESTs; colon; CTL	
	322303; AI357412; Hs.157601; ESTs; colon, pros, fibro, breast; CTL+diag	
	400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.	
	400297; AI127078; Hs.288351; hypothetical protein DKFZp564C; breast, blad, colon, pros; mAb	
30	400303; AW242758; Hs.79136; LIV-1 protein, estrogen regula; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb	
	400843; ; NM_003109; Homo sapiens sortilin; blad; s.m.	
	402076; ; ENSP00000251056; Plasma membrane blad, lung, headnk, cerv, mela, esoph; mAb+diag	
	402901; ; NM_025206; Homo sapiens hypoth; blad; CTL	
	404287; ; FGENESH predicted novel CUB-domain; panc, lung, colon, uter, esoph; mAb+s.m.	
	404682; ; ortholog of mouse polydomain p; panc; diag	
35	404875; ; NM_022819; Homo sapiens phosph; blad; CTL+s.m.	
	404977; ; Insulin-like growth factor 2 (c; blad, ovar, sarc; mAb+diag	
	405033; ; C1002652*gi 544327 sp Q04799 ; blad; s.m.	
	408400; ; kallikrein 8 (neurokinin/ovasin; ovar, uterus; diag	
	408954; M21305; FGENESH predicted novel secrete; angio, blad, fibro, sarc; diag	
40	407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE4299; glo, blad; CTL	
	407792; AI077745; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag	
	407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag	
	407836; T79340; Hs.22575; B-cell CLLymphoma 6, member 1; angio; CTL	
45	407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag	
	408243; Y00787; Hs.524; interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag	
	408367; AK001178; Hs.44424; Homo sapiens orphan neutrophil; mela; mAb+s.m.	
	408369; R38438; Hs.118747; SLC16A2 Solute carrier family 16, member 2; pros, lung, fibro, uter, glo, cerv, ovar; mAb	
	408380; AF123050; Hs.44532; dubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL	
	408482; NM_000676; Hs.45743; adenosine A2B receptor; lung, esoph, headnk, colon; mAb+s.m.	
50	408552; AF436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.	
	408790; AW580227; Hs.47860; neurotrophic tyrosine kinase; lung; mAb+s.m.	
	408908; BE296227; Hs.250522; serine/threonine kinase 15; blad, lung, headnk, stom, colon; s.m.	
	409041; AB033025; Hs.50183; Hypothetical protein, XP_05183; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag	
	409079; WB7707; Hs.82065; Interleukin 6 signal transduct; breast, pros; mAb+s.m.	
55	409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL	
	409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, mela; diag	
	408220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.	
	409420; Z15008; Hs.54451; laminin, gamma 2 (neon 100k; lung, headnk, panc, stom, cerv, esoph, blad; diag	
	409632; W74001; Hs.55279; serine (or cysteine) proteinases; lung, blad, headnk; diag	
60	409683; AI743750; Hs.58306; KIAA1862 protein; renal; CTL	
	409757; NM_001898; Hs.123114; cyclatin SN; panc, stom, lung, blad; diag	
	409889; AW630041; Hs.56937; suppression of tumorigenicity; colon, ovar, pros; mAb+s.m.	
	409893; AW247090; Hs.57101; mitochondrial genome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.	
	409958; AW103354; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag	
65	410001; AB044036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung; diag	
	410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m.	
	410153; BE311928; Hs.15830; hypothetical protein FLJ12891; renal,blad; CTL	
	412074; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL	
	413030; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.	
70	410407; X68830; Hs.63267; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.	
	410418; D31352; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.	
	411274; NM_002776; Hs.69423; kallikrein 10; colon, over, uter, cerv, headnk, blad; diag	
	411411; AA345241; Hs.555950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.	
	411773; NM_006799; Hs.72026; protease, serina, 21 (testislin; ovar, diag	
75	411975; AI918058; Hs.144583; 3'UTR of dead ringer (Drosoph; test, colon; CTL	
	412078; X69695; Hs.73149; paired box gene 8; ovar; CTL	
	412140; AA215691; Hs.73625; Rab6 interacting, kinase-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.	
	412314; AA825247; Hs.356084; G protein-coupled receptor 27; ovar, uter, test; mAb+s.m.	
	412609; Z48804; Hs.74124; ocular albinism 1 (Netheship; mela; s.m.	
	412528; AI972402; Hs.306051; hypothetical protein MGC2848; pros; diag	
80	412709; AL022327; Hs.74518; KIAA0027 protein; glo, sarc; mAb+s.m.	
	412718; AW016610; Hs.818; ESTs; lung, headnk, blad, glo, cerv, sarc; s.m.	
	412959; DB745B; Hs.75090; KIAA0282 protein; glo; CTL+s.m.	
	413048; M33221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb	

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage ; glio, ovar, blad, lung ; diag
 413278; BE563085; Hs.833; interferon- γ -stimulated protein; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela; CTL+s.m.
 413324; VO0571; Hs.75294; corticotropin releasing hormone; blad; diag
 5 413385; M34455; Hs.840; indoleamine-pyrole 2,3 dioxyg; blad, lung, mela, fibro, uter, sarc; s.m.
 413554; AA319146; Hs.75426; secretogranin II (chromogranin; panc, glio; diag
 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
 414555; N08569; Hs.76422; phospholipase A2, group IIa (p; pros; s.m.
 414577; AU065548; Hs.77938; hypothetical protein FLJ20592; angiogenesis; CTL+diag
 10 414774; X02419; Hs.77274; plasminogen activator, urokinase; lung, blad, headnk, panc, stom, ovar, esoph; diag
 414812; X72755; Hs.77367; monokine induced by gamma interleukin; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mela, esoph; diag
 414883; AA926950; Hs.346669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
 414907; X03725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
 414991; C17898; Homo sapiens up-regulated by B; fibro, lung; mAb+diag
 415138; C18368; Hs.295944; tissue factor pathway inhibitor; angio, panc, stom, lung, blad, headnk, cerv, stom, ovar, esoph; diag
 15 415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
 415658; AW957684; Hs.306814; Homo sapiens lysyl oxidase-like; mela; diag
 415689; NM_005025; Hs.76589; serine (or cysteine) proteinases; lung; mAb+diag+s.m.
 415617; U88967; Hs.78867; protein tyrosine phosphatase; lung, glio, headnk, cerv, mela, esoph, fibro; mAb+s.m.
 415929; AA724373; Hs.304950; Homo sapiens mucolipin-3 (MCOLN1; mela; mAb
 20 416091; AF295370; Hs.283082; defensin, beta 3; headnk, esoph, mela; CTL+diag
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient 2); lung, headnk, colon, uter, stom; CTL+s.m.
 416250; AA581368; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
 416530; U62801; Hs.79361; kallikrein 6 (neurokinin, zymo); ovar, uter; diag
 416638; N32538; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mela; mAb+s.m.
 416656; U03272; Hs.79432; fibrillin 2 (congenital contractive; lung, ovar, uter, blad, angio, test, sarc; diag
 416836; D54745; cholecystokinin; pros, EWS, glio ; diag
 416857; AA188775; Hs.292453; FGENESH predicted TM containin; glio; mAb+s.m.
 416966; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
 417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; blad, lung, headnk, cerv, esoph; diag
 417166; AA431323; Hs.42146; Paired box protein Pax-3; mela, sarc; CTL
 417389; BE260954; Hs.82045; midkine (neutrophil growth-promot); ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon, sarc; mAb+diag
 417433; BE270268; Hs.82128; 574 oncofetal trophoblast glyc; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
 35 417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar, mAb
 417866; AW067803; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela; mAb+diag+s.m.
 418030; BE207573; Hs.83321; neurogranin B; glio, psmc; diag
 40 418064; BE387287; Hs.83384; S100 calcium-binding protein; mela; diag
 418281; U09550; Hs.1154; oviductal glycoprotein 1, 120K; uter, ovar; CTL+diag
 418495; U38945; Hs.1174; cyclin-dependent kinase inhib; lung, blad, ovar, headnk, panc, cerv, mela, sarc; s.m.
 418506; AA084248; Hs.372265; Unknown protein for MGC:29843; angio, ovar, glio, uter, lung, blad, panc, mela, sarc; mAb+diag
 418526; BE019020; Hs.85388; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
 45 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk, blad; s.m.
 418678; NM_001327; Hs.87225; cancer-testis antigen (NY-ESO-1; lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
 418738; AW388633; Hs.8682; solute carrier family 7, (catt); angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
 418830; BE513731; Hs.349874; hypothetical protein MGC4816; lung; CTL
 418867; D31771; Hs.89404; msh (Drosophila) homeo box horn; blad; s.m.
 50 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.
 419092; AW160835; Hs.89878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
 419121; AA374372; Hs.89626; parathyroid hormone-like hormone; lung, esoph, headnk, blad; diag
 419171; NM_002848; Hs.89655; protein tyrosine phosphatase; lung; mAb+s.m.
 55 419172; AW338525; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
 419183; U60869; Hs.89663; cytochrome P450, subfamily XXI; blad, lung, headnk, panc; CTL+s.m.
 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
 419235; AW470411; Hs.284833; neurotrypsin; panc, fibro, headnk, lung; mAb+diag
 419452; U33635; Hs.80572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
 60 419508; AW997938; Hs.90796; ATP-binding cassette, sub-famf; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
 419558; U29615; Hs.91093; chitinase 1 (chitotriosidase); lung, fibro, test; mAb+diag
 419704; AA28104; Hs.45057; ESTs; glio; CTL+s.m.
 419723; AL120193; Hs.339810; longevity assurance (LAG1, S. ; glio; mAb+diag
 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mela, sarc; CTL+s.m.
 65 419833; AA251131; Hs.220897; Homo sapiens tryptophanyl-tRNA; fibro, stom, blad, esoph, uter; diag
 420159; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 fl; blad, stom; mAb
 420162; BE378432; Hs.85577; cyclin-dependent kinase 4; lung, mela, sarc; s.m.
 420370; Y13645; Hs.97234; uroplakin 2; blad; mAb
 420440; NM_002407; Hs.97644; mammoglobin 2; ovar, uter, cerv; diag
 70 420602; AF060877; Hs.99236; regulator of G-protein signal; headnk, glio, cerv, mela; CTL+s.m.
 420610; AI683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
 420737; U08096; Hs.99899; CD70 ; tumor necrosis factor ; renal; mAb+s.m.
 420876; AA918425; Hs.177744; FGENES predicted novel protein; panc, blad; s.m.
 421056; AU076725; Hs.101408; branched chain aminotransferas; blad, lung; CTL+s.m.
 75 421110; AJ250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
 421340; F07783; Hs.1369; decay accelerating factor for ; angio, panc, stom; diag
 421378; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mela, esoph; diag
 421471; U09545; Hs.327179; solute carrier family 17 (sod1); renal; mAb+s.m.
 421474; U76352; Hs.104637; solute carrier family 1 (gluta; lung; mAb+diag
 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 80 421552; AF026592; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
 421563; NM_006433; Hs.105806; granulysin; fibro; diag
 421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag
 421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer; breast, panc, lung, omuc; diag

- 421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-famf; lung; mAb+s.m.
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-famf; lung, cerv, headnk, blad; mAb+s.m.
 421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.
 5 422048; NM_012445; Hs.268126; spondin 2, extracellular matri; panc, pros, sarc; diag
 422083; NM_001141; Hs.111258; arachidonate 15-lipoxygenase ; pros; s.m.
 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
 422192; AA305159; Hs.113019; fts485; mela; s.m.
 10 422280; AA315939; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45; lung, blad, test, cerv, headnk, esoph; s.m.
 422303; D80783; Hs.115269; epiregulin; panc, colon, blad; mAb+diag
 422397; AJ223368; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.
 15 422424; AI186431; Hs.296638; prostate differentiation facto; blad, panc, pros, angio, colon, stom, lung, mela; diag
 422578; AF239666; Hs.1545; caudal type homeo box transcr; colon; CTL
 422627; BE336857; Hs.118787; transforming growth factor, bet; colon, renal, sarc; mAb+diag
 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
 20 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uterus, angio, stom, test; s.m.
 422857; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell ; ovar, blad, panc, lung, headnk, colon,stom; CTL+s.m.
 423161; ALD49227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
 423184; NM_004428; Hs.1624; ephrin A1; pros, panc, renal,colon; mAb+s.m.
 25 423242; AL039402; Hs.125783; DEME1 protein; breast, renal, ovar, pros, colon; CTL
 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
 423583; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 423634; AW959908; Hs.1693; heparin-binding growth factor ; lung, blad, headnk, panc; diag
 423673; BE003054; Hs.1685; matrix metalloproteinase 12 (mmp12); blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
 30 423936; U77629; Hs.135639; schaetzle-scuete complex (Drosophila); colon, stom, ovar, CTL
 423961; D13566; Hs.136348; peroxisome (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
 424008; R02740; Hs.137555; putative chemokine receptor, C; blad, headnk, stom, cerv, esoph; mAb+s.m.
 424046; AF027856; Hs.138202; serine (or cysteine) proteinases; headnk, lung, cerv; diag
 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
 35 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
 424411; NM_005208; Hs.146549; crystallin, beta A2; panc, sarc; s.m.
 424502; AF242388; Hs.149585; integrin; lung; s.m.
 424503; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros,angio, blad, lung; mAb+s.m.
 424620; AA101045; Hs.151254; kallikrein 7 (chymotrypsic, St; ovar; diag
 40 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
 424825; AF207069; Hs.153357; procollagen-lynsine, 2-oxoglutar; mela; CTL+s.m.
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene 8); ovar, blad, lung, headnk, panc, stom; s.m.
 424917; A163620B; Hs.96901; hypothetical protein FLJ12049; fibro, uter, ovar; CTL
 45 424943; AU077280; Hs.153924; death-associated protein kinase; fibro; s.m.
 425009; X56288; Hs.154151; protein tyrosine phosphatase, ; renal, fibro; mAb+s.m.
 425071; NM_013989; Hs.154424; delodinase, lodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
 425115; R44684; Hs.123956; downstream of G protein-coupl; glc; mAb+s.m.
 425247; NM_005840; Hs.158324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
 50 425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
 425322; U63630; Hs.155637; protein kinase, DNA-activated; lung, headnk; s.m.
 425535; AB007937; Hs.158287; syndecan 3; mela, glc; mAb+s.m.
 425660; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb
 425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb
 55 425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
 425734; AF056209; Hs.159396; pepfido/glycine alpha-aminidat; lung; s.m.
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
 425842; A1687490; Hs.159623; NK-2 (Drosophila) homolog B; panc, glc; s.m.
 425851; AK001504; Hs.158551; death receptor 6, TNF superfamily; blad, lung, headnk; mAb+s.m.
 60 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
 426998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
 428028; NM_001110; Hs.172026; a disintegrin and metalloprote; blad; mAb+diag
 426215; AW983419; Hs.155223; stanniocalchin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
 428227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
 65 426322; J06088; Hs.2012; transcobalamin 1 (vitamin B12; panc, blad, stom; diag
 428344; H41821; Hs.322489; transcriptional activator of t; glc; CTL+s.m.
 426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
 426451; A190165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
 426514; BE816833; Hs.170196; bone morphogenetic protein 7 ; ovar, colon, blad, lung, cerv; mAb+diag
 70 426600; NM_003378; Hs.171014; VGF nerve growth factor induc; mela, sarc; diag
 426761; A1015709; Hs.172069; PORININ Pro-oncoss receptor ; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
 426812; AF105365; Hs.172613; solute carrier family 12 (pol); renal; mAb+s.m.
 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
 427239; BE270447; Hs.356512; ubiquitin carboxyl protein; lung, blad, test, mela, sarc; CTL+s.m.
 75 427335; AA448542; Hs.278444; G antigen 78; lung, headnk, blad, mela, esoph, sarc; CTL
 427343; AB180044; Hs.176977; protein kinase C binding prote; glc; CTL+s.m.
 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
 427923; AW274357; Hs.301406; FGENESH predicted 11 TM prot; mela; mAb
 427969; NM_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag
 80 428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL
 428179; A1127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
 428187; A1687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
 428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, fauk, lung; diag

- 428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+*s.m.*
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (mig; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+*s.m.*
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
 428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag
 5 428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; *s.m.*
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; *s.m.*
 428484; AF104032; Hs.184601; solute carrier family 7 (cato; lung, blad, headnk, cerv, esoph, glo, uter, stom, colon, mela; mAb+*s.m.*
 428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag
 10 428505; AL035461; Hs.2281; chromogranin B (secretogranin ; panc, lung; diag
 428513; BE220806; Hs.184697; plectin CT; mela, panc, breast stom, headnk; mAb
 428579; NM_005766; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+*s.m.*
 428664; AK001668; Hs.189035; similar to SALL1 (sal) (Drosoph; blad, ovar, pros, lung, stom, test; CTL+*s.m.*
 428698; AA652773; Hs.334838; KIAA1866 protein; breast, colon, lung, blad, headnk, ovar, EWS; mAb
 428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag
 15 428758; AA443988; Hs.98502; CA125 antigen; mucin 16; ovar, cerv, lung, panc, stom, renal; diag
 428778; AK000530; Hs.19326; fibroblast growth factor receptor; ovar; mAb+*s.m.*
 428953; AA306810; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
 428969; AF120274; Hs.184689; artemin; lung, cerv; diag
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG); stom, panc, colon, ovar, fibro; mAb+*s.m.*
 20 429149; AW193360; Hs.197982; Homolog of mouse ADP-ribosylat; glo; mAb+*s.m.*
 429211; AF062693; Hs.198249; gap junction protein, beta 5 ; lung, blad, headnk, cerv, esoph, stom, mela; mAb+*s.m.*
 429263; AA019004; Hs.191396; ATP-binding cassette, sub-fam1; lung; mAb+*s.m.*
 429276; AF055085; Hs.198612; G protein-coupled receptor 51; angi, blad, glo; mAb+*s.m.*
 25 429353; AL117406; Hs.335891; ATP-binding cassette; transport; breast, pros; mAb+*s.m.*
 429547; AW009165; Hs.99376; FGENESH predicted novel secret; panc, headnk, lung, ovar; diag
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung, fibro; mAb+diag
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; *s.m.*
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin); lelo; mAb+*s.m.*
 30 430147; R80704; Hs.234434; babyonenhancer-of-split relate; glo; *s.m.*
 430178; AW449612; Hs.152475; 3'UTR of: schacht-soute complex; colon, stom, ovar; CTL
 430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
 430413; AW842182; Hs.241392; small inducible cytokine A5 (IR; fibro, esoph, mela; diag
 430486; BE062109; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv, esoph; mAb+*s.m.*
 430822; AJ005371; Hs.248017; glycerakdehyde-3-phosphate dsh; mela, sarc; *s.m.*
 35 431130; NM_006103; Hs.2719; HE4; epikidymis-specific, whey; ovar, uter; diag
 431462; AW583672; Hs.266311; granin-like neuroendocrine pep; panc, lung, glo, test; diag
 431515; NM_012152; Hs.258583; EDG-7 (endothelial different; ovar, pros, lung, blad; mAb+*s.m.*
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+*s.m.*
 431629; AA170225; Interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
 40 431630; NM_002204; Hs.266529; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+*s.m.*
 431745; AW972445; Hs.163425; Novel FGENESH predicted cadherin; fibro, ovar, uter; mAb
 431840; AA534908; Hs.2660; POU domain, class 5, transcript; test, renal, blad; CTL
 431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
 45 431858; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
 432101; AI918950; Hs.123642; EphA3; pros, panc, EWS sarc; *s.m.*
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+*s.m.*
 432186; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL
 432201; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung ; mAb+diag+*s.m.*
 50 432579; AF043244; Hs.278439; nucleolar protein 3 (apoprote; renal; CTL
 432586; AJ222474; Hs.278461; matrin 3; panc, breast, sarc; diag
 432616; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
 432829; W63077; Hs.57772; ESTs; blad; CTL+*s.m.*
 432874; W84922; Hs.279551; melanoma Inhibitory activity; panc, stom, mela, sarc; diag
 55 432990; AL036071; Hs.279599; tumor necrosis factor receptor; pros, renal; mAb+*s.m.*
 433001; AF217513; Hs.279905; clone HQ0310p1; colon, breast, lung, blad, cerv, uter, test, mela; *s.m.*
 433447; U29195; Hs.3261; neuronal pentraxin III; mela, esoph, colon, renal; diag
 433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; *s.m.*
 433867; AK000596; Hs.3618; hippocalcin-like 1; renal; CTL
 60 434205; AW136973; Hs.362915; ESTs, Weakly similar to 869890; colon, lung, stom; CTL+*s.m.*
 434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; *s.m.*
 434293; NM_004446; Hs.3796; EphB6; blad, pros; *s.m.*
 435013; H91923; Hs.110024; NM_020142; Homo sapiens NADHtub; renal, lung, sarc; CTL
 435472; AW972330; Hs.283022; triggering receptor expressed ; glo; mAb
 65 435505; AF200492; Hs.211238; Interleukin-1 homolog 1; lung, headnk; diag
 436466; AW292677; Hs.248122; melanin-concentrating hormone ; mela, glo; mAb+*s.m.*
 436480; AJ271643; Hs.87489; putative acid-sensing ion chan; glo; mAb+*s.m.*
 436481; AA379587; Hs.6199; HSPC160 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; *s.m.*
 436576; AI58213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+*s.m.*
 70 436606; AI620980; Hs.192371; down syndrome critical region ; blad, lung, sarc; CTL+*s.m.*
 436895; AF037335; Hs.5338; carbonic anhydrase XII; breast, renal, ovar; glo; mAb+*s.m.*
 436951; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon ; CTL
 436982; AB018306; Hs.5378; spondin 1, (spondin) extrace; ovar, fibro; diag
 437016; AU076916; Hs.5398; guanine monophosphatase synthetase; lung, blad, cerv, esoph, colon, headnk; *s.m.*
 75 437044; AL035864; Hs.69517; differentially expressed FA; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
 437789; AI581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
 437852; BE001836; Hs.256197; putative GPCR; blad, lung; mAb+*s.m.*
 439380; TD6430; Hs.6194; chondroitin sulfate proteoglyc; glo, mela; diag
 436549; BE386801; Hs.21856; trinucleotide repeat containin; mela, sarc; CTL+diag
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, 5; uter, stom, pros, fibro; mAb
 439223; AW238299; Hs.250518; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
 439477; W630813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+*s.m.*
 80 439569; AW602168; Hs.222399; CEGP1 protein; breast, pros, blad; diag
 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+*s.m.*

- 439738; BE246502; Hs.9598; serna domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
 439978; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containin; blad, ovar, lung, headnk, test; s.m.
 440065; W03478; Hs.288331; Homo sapiens Fc receptor homot; mela; diag
 440304; BE159984; Hs.125395; hepatitis A virus cellular res; renal, colon, blad; mAb+s.m.
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glo, ovar, uter, renal, hepC; mAb+diag
 440872; AF083811; Hs.7345; MAD1 (mitotic arrest deficient); mela; s.m.
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog; lung, blad, headnk, test, mela, esoph; s.m.
 442117; AW684964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
 442133; AW874138; Hs.129017; ESTs; type la transmembrane p; ovar, uter, mAb
 442275; AW449467; Hs.54795; Homo sapiens secretoglobin, fa; fibro; diag
 442652; AW05163; Hs.201378; Homo sapiens cDNA FLJ40427 fib; fibro, ovar, uter; CTL
 443105; X95753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
 443426; AF098158; Hs.9325; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
 443693; AF169312; Hs.9613; PPAR(gamma) angiotropolin relat; renal; diag
 443846; AI085198; Hs.164226; Thrombospondin 1; anglo, panc, uter; diag
 443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
 443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
 444008; BE395085; Hs.334762; type II transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
 444090; S89115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
 444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glo, test, mela; s.m.
 444381; BE387335; Hs.28713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, over, stom, uter, renal, anglo, test, mela, esoph, sarc; CTL+diag
 444488; AW192879; Hs.356660; ancient conserved domain prote; renal; mAb+s.m.
 444527; NM_005408; Hs.11383; small inducible cytokine subf; fibro, esoph; diag
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-assoc; lung, blad, headnk, cerv; mAb+diag
 444783; AK001468; Hs.62180; exillin (*Drosophila* Scrapt hum); over, lung, blad, headnk, punc, cerv, stom, uter, colon, esoph; CTL+s.m.
 445147; AK001058; Hs.12680; a disintegrin-like and metallo; punc, headnk, stom, lung, esoph, sarc, colon; diag
 445637; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
 445891; AW391342; Hs.199460; DPCR1 protein; stom, punc, esoph, omuc, esoph; mAb
 445895; D29854; Hs.13421; KIAA0056 protein; pros; CTL
 446051; BE048061; Hs.37064; ephrin-A3; colon, breast; mAb+diag
 446163; AA025880; Hs.25252; prolatin receptor; breast, cerv, uter; mAb+s.m.
 446341; ALD40763; Hs.310735; FGENESH prediction similar to ; mela; mAb+s.m.
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; over, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
 446921; AB012113; Hs.16530; small inducible cytokine subf; breast, punc, headnk, lung, fibro, mela; diag
 447033; AJ357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, over, lung, panc, sarc; CTL+diag
 447072; DE1594; Hs.17279; tyrosyl/protein sulfotransferas; glo, panc; CTL+s.m.
 447131; NM_004585; Hs.17466; retinoid acid receptor respond; renal, breast, stom, lung, mela, over; mAb+s.m.
 447208; BE315281; Hs.237971; hypothetical protein MGCG627; esoph, stom, colon; CTL+diag
 447269; NM_004861; Hs.17958; cerebroside (3'-phosphoacyl)enyl; renal; CTL
 447342; AI199268; Hs.19322; Homo sapiens; Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
 448243; AW369771; Hs.367688; Integrin, beta 8; over, uter, lung, stom, headnk, glo, panc ; mAb+s.m.
 448610; NM_006157; Hs.21602; nel (chicken)-like 1; mela, sarc; diag
 448733; NM_005628; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
 448844; AS81519; Hs.177164; FGENESH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
 449032; AA045573; Hs.22900; nuclear factor (erythroid-derived; colon, test, stom; CTL+s.m.
 449048; Z45051; Hs.22920; similar to S68401 (catle) glu; panc, over, uter, glo, headnk, lung, sarc; mAb
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
 449523; NM_000579; Hs.64443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
 449720; AA311152; Hs.287098; hypothetical protein FLJ21562; colon; CTL
 449722; BE280074; Hs.23950; cyclin B1; headnk, blad, lung, pano, anglo, test, mela, esoph; s.m.
 450001; NM_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.
 450375; AA009647; Hs.352537; a disintegrin and metalloprote; breast, over, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
 450701; Hs.39960; Hs.288467; hypothetical protein XP_098161; lung, headnk, panc, breast, stom, over, esoph, colon, sarc; mAb+diag
 450728; AW204600; Hs.355462; HUMPSPIBA Human pulmonary surfa; fibro, lung; s.m.
 450831; N25156; Hs.25548; tumor necrosis factor receptor; lung, renal; mAb+s.m.
 450983; AA305384; Hs.257470; ERO1 (S. cerevisiae)-like; blad, lung, over, panc; diag
 451310; AW250551; Hs.28213; Human DNA sequence from clone ; colon, panc; CTL
 451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb
 451637; R56631; Hs.26560; reinoif X receptor, gamma; male; CTL+s.m.
 451668; Z43948; Hs.328444; cartilage acidic protein 1; blad, over, lung; mAb+diag
 451938; UB0456; Hs.27311; single-minded (*Drosophila*) hom; pros; CTL
 451979; F08972; Hs.27372; endothelial tyrosine kinase (E; anglo; CTL+s.m.
 451988; AF263920; Hs.27410; papillomavirus regulatory fact; renal; CTL
 452017; AF103932; Hs.27495; prostate cancer associated pro; pros; s.m.
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; over; mAb+s.m.+diag
 452180; H26735; Hs.91668; Homo sapiens clone PP1498 unk; breast, stom, panc; mAb
 452194; AI694413; Hs.373599; olfactory receptor, family 2; stom, panc, renal, colon, mela; fibro; mAb+s.m.
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
 452281; T03500; Hs.28792; Homo sapiens cDNA FLJ11041 fib; breast, headnk, panc, stom, lung, esoph, fibro; diag
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-1; blad, breast, punc, headnk,stom, lung, leuk, renal, esoph; diag
 452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, over, stom, uter, punc; mAb
 452838; U65011; Hs.30743; preferentially expressed antigen; lung, over, breast, mela, test, esoph, renal, sarc; CTL
 452862; AW378065; Hs.8887; ADAMTS2 (a disintegrin-like e; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
 453498; AAA442103; Hs.33084; soluta carrier family 2 (facil; renal, pros; mAb+s.m.

453837; AL138387; Hs.256126; baculoviral IAP repeat-contain; renal, mela, sarc; s.m.
 453968; AA847843; Hs.02711; High mobility group (nonhistone; lung, uter, blad, test; CTL+s.m.
 456546; AI690321; Hs.203845; KCNK15 potassium channel, subf, over; mAb+s.m.
 456862; NM_002448; Hs.1494; mesh (Drosophila) homeo box horn; uter, ovar; CTL
 457133; M54966; Hs.351221; v-K-ras2 Kirsten rat sarcoma; panc; s.m.
 457489; AI693815; Hs.127179; cryptic gene; panc, pros, lung; diag
 457819; AA057484; Hs.36405; FLJ20522 Hypothetical protein; lung, cerv, headnk; mAb+diag
 458079; AJ796870; Hs.361220; Homo sapiens similar to RIKEN; mela, fibro, sarc; mAb
 458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

10

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

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414991 1785138_1 D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

30

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9873-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175428-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9255298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

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Table 3A provides preferred disease indications and preferred utilities for about 2700 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number

ExAcct: Exemplar Accession number

UnigeneID: Unigene ID number

Unigene Title: Unigene gene title

50

Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), anglo (blood vessel diseases), EWS (bone diseases), glo (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), hlio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)

55

Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAcct; UnigeneID; Unigene Title; Disease; Utility:

60

100125; R02740; Hs.137556; putative chemokine receptor; G; blad; mAb+s.m.

100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb

100147; D1366; Hs.136348; perifosin, (OSF-2αs); breast, colon, blad, lung, fibro, panc; mAb+diag

100241; BE273648; Hs.32983; cadherin 6, type 2, K-cadherin; blad; mAb

100298; D49493; Hs.2171; growth differentiation factor; EWS; diag

100335; AW247529; Hs.6793; platelet-activating factor acp; breast, lung, blad; s.m.

100365; A1878827; Hs.79284; mesoderm specific transcript (-); colon, pros; diag

100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.

100405; AW291507; Hs.62733; nitrogen 2; anglo; diag

100420; DB8983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, anglo, leuk; diag

100448; AF234887; Hs.57652; caudin, EGF LAG seven-pass G; breast; mAb+s.m.

100452; D87742; Hs.241552; KIAA0268 protein; pros; diag

100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (ε); lung; CTL+s.m.

100654; A03758; Hs.184411; NM_000477; Homo sapiens albumin; pros; diag

100655; A03759; Hs.184411; Empirically selected from AFFX; pros; diag

100666; L05424; Hs.169610; CD44 antigen (homing function); lung, breast; mAb

100684; A1893237; Hs.193969; runt-related transcription factor; ovar; CTL+s.m.

100930; J04128; Hs.822269; progastrulin-associated endomet; lung; diag

101063; D54745; Hs.80247; cholecystokinin; pros, EWS; diag

70

101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.

101104; AW862256; Hs.169268; neuropeptide Y receptor Y1; breast, EWS; mAb

101192; BE247295; Hs.78452; solute carrier family 20 (phos angio); mAb+s.m.

101193; L20681; Hs.152213; wingless-type MMTV integration; blad, lung; diag

101249; L18954; Hs.1904; protein kinase C, iota; ovar; s.m.

75

- 101261; D30857; Hs.82353; protein C receptor, endothelia; angio; mAb+s.m.
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA); pros; mAb+s.m.
 101431; BE185289; Hs.1076; small proline-rich protein 1B ; lung, blad; diag
 101447; M21305; gb; Human alpha satellite and s; angio, blad; diag
 5 101461; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; diag
 101485; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, ovar; mAb
 101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb
 101528; NM_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb
 101543; M31166; Hs.2050; pentraxin-related gene, rapidly; angio, ovar; diag
 10 101545; BE246154; Hs.154210; endothelia differentiation, s; angio; mAb+s.m.
 101560; AW958272; Hs.347326; intercellular adhesion molecule; angio; mAb
 101626; M57399; Hs.44; pleiotrophin (heparin binding ; lung; diag
 101649; AW959905; Hs.1690; heparin-binding growth factor ; lung, blad; diag
 10 101714; MG8874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
 15 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (breast, pros, blad, lung; mAb+CTL
 101741; NM_003199; Hs.326198; transcription factor 4; angio; CTL+s.m.
 101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, carv; mAb
 101759; M80244; Hs.184601; solute carrier family 7 (cation; lung, glio, blad, headnk; mAb+s.m.
 10 101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.
 101804; M86699; Hs.16940; TTK protein kinase; over, lung, blad, carv; CTL+s.m.
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
 10 101809; M86849; Hs.323733; gap junction protein, beta 2 ; colon, blad, lung, panc, headnk; mAb
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gl; over, pros; mAb
 20 101845; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, carv; mAb+s.m.
 101851; BE260964; Hs.82045; midkine (neutrie growth-promot; lung, blad, ovar, breast, panc; mAb+diag
 102009; BE245149; Hs.82543; protein tyroline kinase 9; over; s.m.
 102012; BE289035; Hs.118400; singed (Drosophila)-like (sea ; angio; diag
 102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 30 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
 102125; NM_008456; Hs.288215; sialyltransferase; breast, lung, ovar; s.m.
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 102154; U17760; Hs.75517; laminin, beta 3 (nican (125kD); lung, blad, headnk; diag
 35 102176; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag
 102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; over, lung, fibre; diag
 102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.
 102208; U22961; Hs.184411; gb; Human mRNA clone with simili; pros; diag
 40 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
 102297; NM_001504; Hs.193252; G protein-coupled receptor 9; breast; mAb
 102304; AF015224; Hs.46452; gammagloblin 1; breast; diag
 45 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; over, lung, blad; diag
 102348; U37519; Hs.87539; aldehyde dehydrogenase 3 fam1; lung, blad; s.m.
 102380; U40434; Hs.155081; mesothelin; ovar; diag
 102394; NM_003816; Hs.2442; a disintegrin and metalloprotein; panc; s.m.
 102455; U48705; Hs.75562; discoidin domain receptor fam1; breast; mAb
 50 102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
 102522; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb
 102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuc; CTL+s.m.
 102610; U65011; Hs.30743; preferentially expressed antif; lung, ovar, CTL
 102623; AW249265; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL
 102669; U71207; Hs.29279; eyes absent (Drosophila) homot; lung, pros; CTL+s.m.
 55 102696; BE540274; Hs.238; forkhead box M1; lung, blad; s.m.
 102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb
 102742; UT9293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar; diag
 102745; AW753885; Hs.74376; octadecenoate related ER locali; EWS; diag
 102803; H48299; Hs.26110; over; mAb
 60 102829; NM_006183; Hs.80962; neuroleuken; lung, ovar, headnk; diag
 102831; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
 102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 102898; NM_002205; Hs.449609; Integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+e.m.
 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
 65 102917; AL016712; Hs.287797; Integrin, beta 1 (fibronectin; angio; mAb
 102927; BE512730; Hs.85114; keratin 18; ovar; diag
 102968; AL076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 70 103003; AI910275; Hs.350470; trefoil factor 1 (breast cancer; breast, panc; diag
 103021; BE001586; Hs.85266; Integrin, beta 4; lung blad; mAb
 103038; M13508; Hs.83169; matrix metalloproteinase 1 (in; angio, colon, blad, lung, leuk, over, headnk, fibro, panc, stom; mAb+diag+s.m.
 103037; BE018302; Hs.2894; placental growth factor, vaso; angio; diag
 103050; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, over, panc; mAb+diag+s.m.
 75 103080; AU077231; Hs.82332; cyclin D1 (PRAD1; parathyroid ; breast, EWS; diag
 103095; NM_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb
 103111; NM_005103; Hs.2719; epilidymis-specific, whey-acid; over, uter; diag
 103119; X63628; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
 103206; X72755; Hs.77367; monokine induced by gamma int; breast, lung; diag
 80 103210; X72925; Hs.89752; desmocolin 1; pros; mAb
 103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin; angio, fibro; mAb+s.m.
 103299; NM_005755; Hs.184942; G protein-coupled receptor 64; over; mAb+s.m.
 103312; Y12642; Hs.3185; lysosomat; lung, blad; mAb
 103365; X90908; Hs.74126; fatty acid binding protein 6 ; blad; diag

103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnck; diag
 103567; BE270265; Hs.82128; ST4 oncofetal trophoblast glyc; breast, blad, lung; mAb
 103594; A1368680; Hs.816; SRY (sex determining region Y); lung, glo; s.m.
 5 103692; AW137912; Hs.227583; Homo sapiens chromosome X map ; angio; mAb+s.m.
 103739; AA115173; gb:zn30d02.s1 Stratagene neuro; pros; s.m.
 103767; BE244667; Hs.348998; CGI-100 protein; angio; diag
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, ornut; mAb+diag
 104052; NM_002407; Hs.97644; mammaglobin 2; ovat; diag
 10 104115; AF183810; Hs.26102; opposite strand of trichorh; breast; mAb
 104252; AF002246; Hs.210863; cell adhesion molecule with fib; ovat; diag
 104308; AA129551; Hs.8783; hypothetical protein FLJ22724; ovat; diag
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 fis; colon; diag
 15 104542; R28957; gb:F1-1178D 22 week old human ; pros; diag
 104608; AF143857; Hs.337588; ESTs; Moderately similar to S6; blad; mAb
 104659; AW969769; Hs.100343; ESTs; EWS; diag
 104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; eter, colon, pros; mAb
 104667; AI239923; Hs.63931; dachshund (*Drosophila*) homolog; breast, pros, colon; diag
 20 104699; AA420450; Hs.380068; Plakophilin; lung; diag
 104691; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
 104764; AI039243; Hs.278586; ESTs; angio; diag
 25 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
 104877; AI138635; Hs.22958; intron of VEGFR; renat; diag
 104888; AW939591; Hs.5840; mucin 13, epithelial transmemb; colon, stom, eter; mAb+s.m.
 104919; AA026880; Hs.262525; Homo sapiens cDNA FLJ13603 fis; breast, cerv, eter; mAb+s.m.
 104943; AF072873; Hs.114218; fizzled (*Drosophila*) homolog ; ovat; mAb+s.m.
 30 104954; AW250651; Hs.262113; Human DNA sequence from clone ; colon; diag
 104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL
 105012; AF098158; Hs.9329; chromosome 20 open reading fr; colon, lung, blad; CTL
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
 105039; AS087305; Hs.36475; ESTs; breast; diag
 105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 35 105149; BE089288; Hs.8956; Homo sapiens cDNA FLJ12024 fis; pros; diag
 105152; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
 105263; AW389633; Hs.6652; solute carrier family 7, (catt); angio, lung, ovar, blad, pancreas; mAb+s.m.
 105298; BE387790; Hs.26389; hypothetical protein FLJ20287; ovar, lung; diag
 105301; AW352367; Hs.7457; MAGE1 protein; EWS; diag
 40 105316; AI671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb
 105329; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.
 105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 105370; AF178274; Hs.22791; transmembrane protein with EGF; pros ; mAb+s.m.
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
 45 105503; AW953624; Hs.31707; ESTs; Weakly similar to *WEW4* Y; pros, breast, colon; CTL+s.m.
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
 105516; AK001289; Hs.30738; hypothetical protein FLJ10407; ovar; diag
 105564; BE616684; Hs.268042; hypothetical protein FLJ14299; breast; diag
 105645; AW294631; Hs.361270; ESTs; pros; diag
 50 105715; BE621800; Hs.29444; putative small membrane protel; colon; diag
 105743; BE248502; Hs.9598; sema domain, Immunoglobulin do; breast, lung; mAb+s.m.
 105748; AW151952; Hs.46679; hypothetical protein FLJ20739; breast; CTL+s.m.
 105777; RA2765; Hs.23056; ESTs; breast; diag
 105782; HD9748; Hs.57987; B-cell CLL/lymphoma 11B (zinc ; EWS; CTL+s.m.
 55 105826; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
 105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
 106000; AW194428; Hs.20728; ESTs; breast; diag
 106012; AI240665; Hs.352537; ESTs; breast, lung; diag
 106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
 106066; AW274357; Hs.301406; hypothetical protein PP3501; mela; CTL+s.m.
 106111; AW875398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.
 106124; H93366; Hs.7587; branched chain aminotransferas; angio; s.m.
 60 106155; AA25414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 fis; colon; diag
 106414; BE568205; Hs.28827; mitogen-activated protein kinase; breast; s.m.
 106448; Z42061; Hs.27004; ESTs; pros; diag
 106533; AL134708; Hs.145998; ESTs; EWS; diag
 65 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
 106579; AA456135; Hs.23023; ESTs; pros; diag
 106592; NM_014400; Hs.11950; GPI-anchored metastasis-assoc; lung, blad, headnck; mAb+diag
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 fis; ovar; diag
 106793; H94997; Hs.16450; ESTs; angio; diag
 70 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
 106906; AA861271; Hs.222024; transcription factor BMAL1; lung, blad; diag
 106990; AA280722; Hs.24758; ESTs; Weekly similar to 138022; breast; diag
 107036; AI973016; Hs.15725; hypothetical protein SB9148; pros; diag
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
 107105; AW963419; Hs.155223; stanniccalcif 2; breast; diag
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
 107151; AW378055; Hs.8887; ADAMTS2 (a disintegrin-like s; breast, colon, leuk, lung, blad; mAb+diag
 80 107216; DS1069; Hs.211579; melanoma cell adhesion molecul; angio; diag

- 107248; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.
 107284; NM_005629; Hs.187958; solute carrier family 6 (neuro); lung; mAb+s.m.
 107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
 107901; L42612; Hs.335952; keratin 6B; breast, blad, lung; diag
5
 107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
 108055; SS9002; Hs.234773; Homo sapiens cDNA: FLJ22281 f1; ovar; CTL+s.m.
10
 108153; AW519204; Hs.40808; ESTs; pros; diag
 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 108242; AA062746; Hs.355244; gb:zmu03g12.s1 Stratagene clone; pros; diag
 108282; AA065142 ; gb:zmu50h11.r1 Stratagene fibro; pros; diag
15
 108505; AA083376 ; gb:zn09g08.s1 Stratagene hNT n; pros; diag
 108679; AA115963; Hs.323423; ESTs, Moderately similar to B ; pros; diag
 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
 108732; AA258888; Hs.107476; ATP synthase, H+ transporting;; pros; s.m.
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
 108828; AK001693; Hs.273344; DKFZP564O0453 protein; breast; diag
 108860; AA133334; Hs.816; ESTs; lung; s.m.
20
 108001; AI056548; Hs.72116; hypothetical protein FLJ20992; angio; CTL+diag
 109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 109077; AF732617; Hs.182362; ESTs; blad; diag
 109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
25
 109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
 109166; AA219591; Hs.73825; RAB6 interacting, kinase-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.
 109220; AW958181; Hs.189998; ESTs; pros; diag
30
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
 109292; AW976746; Hs.188662; KIAA1702 protein; pros; CTL+s.m.
 109454; AA232255; Hs.2955232; ESTs, Moderately similar to A4; ovar; diag
 109456; AW956580; Hs.42659; ESTs; angio, panc; diag
35
 109514; AA234087; Hs.262246; ESTs, Weakly similar to S72482; breast ; diag
 109530; AA908645; Hs.19897; KIAA1694 protein; pros; CTL+s.m.
 109648; H17800; Hs.7154; ESTs; ovar; diag
 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
40
 110009; BE075297; Hs.6814; ESTs, Weakly similar to A4392; breast, colon; diag
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 110240; AI668594; Hs.176568; ESTs, Weakly similar to CPAY_H; breast; diag
45
 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
 110675; HB9365; Hs.249159; adrenergic, alpha-2A-, receptor; pros; mAb+s.m.
 110726; AA737108; Hs.32250; ESTs, Moderately similar to D7; EWS; s.m.
 110844; AT740792; Hs.167531; methylcrotonyl-Coenzyme A car; pros, pros; s.m.
50
 110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
 110971; AT80098; Hs.21411; ESTs; pros; diag
55
 111057; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 111179; AK000136; Hs.10760; espin (LRR class 1); breast, colon; CTL+s.m.
 111185; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad; mAb+diag
 111223; AB852773; Hs.334838; KIAA1866 protein; breast, colon, lung, EWS; mAb
60
 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
 111367; BE314949; Hs.37128; hypothetical protein FLJ23308; breast; diag
 111384; N94608; Hs.288699; HSCAF6 protein; breast; diag
 111900; AF131784; Hs.25318; Homo sapiens clone 25194 mRNA ; breast; diag
65
 111929; AF027203; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 112134; RA1823; Hs.7413; ESTs; calsyntenin-2; breast, EWS; diag
 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.
 112283; L14551; Hs.20952; ATPase, Ca++-transporting, plasma membrane; ovar; mAb
 112287; AB033064; Hs.236463; KIAA1238 protein; breast; diag
 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
70
 113003; AW292315; Hs.7215; ESTs; EWS; diag
 113021; AL122055; Hs.129830; KIAA1028 protein; pros; s.m.
 113047; AI571940; Hs.7549; ESTs; breast, colon; diag
75
 113073; M39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
 113168; AW002353; Hs.337629; gb:wu61d05x1 NCL_CGAP_GC8 Horn; ovar; diag
80
 113195; HB3265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
 113230; T61430; ; gb:yco06e03.s1 Stratagene lung ; blad; diag
 113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 113374; T79928; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
 113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb
75
 113471; AI765990; Hs.16341; MAWD binding protein; pros; diag
 113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 f1; colon; diag
 113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros; diag
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-1); breast; diag
 114251; H16261; Hs.21948; ESTs; breast; diag
 114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
 114452; AI369275; Hs.243010; Homo sapiens cDNA FLJ14445 f1; angio; diag
 114480; BE066778; Hs.151678; UDP-N-acetyl-alpha-D-galactosamine; breast; s.m.
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 114540; AI904232; Hs.75323; prothrombin; breast; diag
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus laevis); breast, pros; diag

- 114587; AF086009; Hs.298398; gb:Homo sapiens full length in; colon; diag
 114724; R64730; comp; Hs.165986; DEADDH (Asp-Glu-Ala-Asp/Hs) b; ovar; CTL+s.m.
 114766; AF212848; Hs.182339; est homologous factor; pros, breast, colon; CTL+s.m.
 114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
 114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag
 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
 114965; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; diag
 115060; AF052693; Hs.198249; gap junction protein, beta 5 ; lung, blad, headnk; mAb+s.m.
 115221; AW365434; Hs.79741; hypothetical protein FLJ10118; ovar; diag
 115239; BE251328; Hs.73291; hypothetical protein FLJ10981; colon; diag
 115291; BE545072; Hs.122579; hypothetical protein FLJ10481; ovar, lung; CTL+s.m.
 115412; AW13168; Hs.372382; ESTs; Weakly similar to I38022; pros; diag
 115536; AK001468; Hs.62180; anilin (*Drosophila* Scraps hom); ovar, lung, blad, headnk, panc, cerv, stom, uter, colon; CTL+s.m.
 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
 115675; W87707; Hs.92065; interleukin 6 signal transduce; breast; pros; mAb+s.m.
 115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio, glo; mAb
 115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros, breast, colon; CTL+s.m.
 115819; AA486620; Hs.41135; endomucin-2; engio; diag
 115827; AA428000; Hs.263072; actin related protein 2/3 comp; angio; diag
 115844; AI373052; Hs.332938; hypothetical protein MGC5370; pros; diag
 115854; NM_005755; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 115892; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
 115909; AW872527; Hs.59761; ESTs; Weakly similar to DAP1_H; ovar, lung; diag
 115947; R47478; Hs.94761; KIAA1691 protein; colon; diag
 115978; AL035864; Hs.69517; cDNA for differentially express; lung, blad, breast, pros, ovar, headnk; CTL
 116003; BE275469; Hs.68493; Down syndrome critical region ; colon; mAb
 116011; AL359053; Hs.57664; Homo sapiens mRNA full length ; breast; diag
 116028; H69799; Hs.42644; fibroedatin-like; ovar, lung; diag
 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 116202; BE159395; Hs.294092; ESTs; pros; diag
 116238; AV660717; Hs.47144; DKFZP588N0819 protein; ovar; diag
 116301; AW969706; Hs.293332; ESTs; EWS; diag
 116334; AL038450; Hs.48948; ESTs; pros; diag
 116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag
 116393; AI972402; Hs.305051; hypothetical protein MCC2848; pros; diag
 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
 116401; AW893940; Hs.59658; ESTs; ovar; diag
 116416; AW753876; Hs.39982; ESTs; ovar; diag
 116470; AI272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag
 116483; AI346201; Hs.76118; ubiquitin carboxy-terminal es; angio, lung; s.m.
 116610; D801449; Hs.184841; ESTs; pros; diag
 116732; AW152225; Hs.163899; ESTs; Weakly similar to I38022; colon; diag
 116767; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb
 116862; H79877; :gb:y76j10.s1 Soares fetal lv; pros; diag
 117027; AW085208; Hs.130093; ESTs; breast ; diag
 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fis; breast, colon, pros; diag
 117284; AI0001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung; mAb+diag
 117367; AI041793; Hs.425202; ESTs; breast ; diag
 117412; N32536; Hs.42645; solute carrier family 16 (mono; breast, ovar ; mAb+s.m.
 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 117553; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk ; diag
 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
 117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros ; diag
 117984; AF189723; Hs.106776; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb
 118049; N53145; :gb:y5509.s1 Soares fetal lv; pros; diag
 118314; N48580; Hs.46692; ESTs; blad, lung; diag
 118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.
 118368; N64339; Hs.48958; gap junction protein, beta 6 ; lung, blad; mAb
 118417; AF080229; :gb:Human endogenous retrovirus; pros; s.m.
 118472; AL157645; Hs.173179; bromodomain and PHD finger con; breast; diag
 118511; N75620; Hs.43157; ESTs; angio; diag
 118901; AW292577; Hs.94445; ESTs; breast; diag
 118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 119018; AA631143; Hs.278695; human protein mRNA, co; pros, pros; diag
 119036; RS5872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb
 119073; BE245360; Hs.46514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.
 119082; AF252297; Hs.91646; cytochrome P450 retinoid metab; EWS; diag
 119126; RA5175; Hs.117183; ESTs; pros, breast, colon; diag
 119279; N57658; Hs.48029; EST; breast; diag
 119307; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 119478; AI624342; Hs.179082; ESTs; breast; diag
 119617; AA516531; Hs.55999; NK homeobox (*Drosophila*), fam; pros; diag
 119743; AA947552; Hs.58086; branched chain aminotransfase; ovar; s.m.
 119771; AI905637; Hs.348410; AI905687; IL-BT095-190199-019 B; breast; diag
 119780; NM_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.
 119789; BE393946; Hs.50915; kallikrein 5; ovar; diag
 119845; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.
 119940; AL060997; Hs.272531; DKFZP588B0319 protein; pros; diag
 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag
 120132; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 120147; AI917116; Hs.348941; hemoglobin, beta; EWS; diag

120206; H26736; Hs.91668; Homo sapiens clone PP1498 unk; breast ; mAb
 120242; AW969587; Hs.86368; ESTs; blad; diag
 120328; AA923278; Hs.290905; ESTs; Weakly similar to proteas; pros; s.m.
 120438; AW015242; Hs.99468; ESTs; Weakly similar to YK54_Y; ovar; diag
 120471; AA251944; Hs.104058; CGI-29 protein; colon; diag
 120486; AW368377; Hs.137659; tumor protein 63 kDa with stn; lung, blad, headnk; diag
 120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 120624; AW407987; Hs.1733518; M-phase phosphoprotein homolog; breast; s.m.
 120830; AI568170; Hs.97600; ESTs; EWS; diag
 10 120977; AA398155; Hs.97600; ESTs; breast; ovar; diag
 121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad; mAb
 121231; AA814948; Hs.98343; ESTs; Weakly similar to ALUC_H; EWS; diag
 121335; AA404418; ; gb:zw37e024.1 Soares_total_fet; angio; diag
 121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb
 121457; W07404; Hs.1026568; hypothetical protein FLJ22055; colon; diag
 121619; AA526339; Hs.178062; ESTs; Weakly similar to phosph; EWS; s.m.
 121710; AF163474; Hs.95744; prostate androgen-regulated tr; pros; diag
 121721; AL047051; Hs.199981; ESTs; Weakly similar to ALU1_H; pros; diag
 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
 121748; BE536911; Hs.234545; hypothetical protein NUF2R; breast; diag
 121779; AW513143; Hs.98357; SRY (sex determining region Y); ovar; diag
 121791; AA815378; Hs.293317; ESTs; Weakly similar to GGC1_L; blad, headnk, lung, ovar; mAb+CTL
 121792; AW569726; Hs.93381; ESTs; Weakly similar to sefine; EWS; diag
 121913; AI249366; Hs.98558; ESTs; protease inhibitor 15 f; breast; pros; s.m.
 121920; AA428300; ; gb:zw1bb02.s1 Soares ovary lum; ovar; uter, cerv; diag
 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 122520; AW951324; Hs.1733609; pregnancy specific beta-1-glyc; colon; diag
 122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB); breast; diag
 122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.
 30 122969; AW821252; Hs.104336; hypothetical protein; ovar; diag
 123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.
 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc ; lung; diag
 123137; AI073913; Hs.100886; ESTs; Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
 123158; AF161426; Hs.218529; hypothetical protein; breast; diag
 123160; AA468587; Hs.284235; ESTs; Weakly similar to I38022; lung; diag
 123169; AI950087; Hs.369628; gb:wg05c022.x1 NCI_CGAP_Kid12_H; ovar; diag
 123209; AW968843; Hs.203270; ESTs; Weakly similar to ALU1_H; pros; diag
 123308; C14187; Hs.157208; ESTs; EWS; diag
 123339; AW188464; Hs.101615; ESTs; ovar; diag
 40 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
 123494; AW179019; Hs.112110; mitochondrial ribosomal prote; ovar; diag
 123520; AA608550; ; gb:se53d12.81 Strategene lung ; pros; s.m.
 123533; AA608751; ; gb:se56h07.s1 Strategene lung ; colon; diag
 123619; AA602954; Hs.366318; gkxno97c02.s1 NCI_CGAP_Pr2 Hom; breast; CTL+s.m.
 123689; AA399323; Homo sapiens plch-2 protein n; ovar; diag
 123709; AA706910; Hs.112742; ESTs; breast; diag
 123828; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
 123972; T46848; Hs.70337; immunoglobulin superfamily, mem; ovar; diag
 50 124006; AI147155; Hs.279727; ESTs; homologus of PEM-3 [Cion]; breast, angio, lung, ovar, EWS; diag
 124058; BE387335; Hs.283713; ESTs; Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
 124153; AI077333; Hs.160493; erythrocyte membrane protein b; pros; mAb
 124352; AA640891; Hs.102400; ESTs; breast, pros, ovar, lung; diag
 124526; NG2098; Hs.293185; ESTs; Weakly similar to JC7328; pros; mAb+s.m.
 124579; AI683815; Hs.127179; cryptic gene; panc; diag
 124777; R41933; Hs.140237; ESTs; Weakly similar to ALU1_H; pros, breast; diag
 125103; AA570056; Hs.122730; ESTs; Moderately similar to K; colon; mAb
 125154; W38419; ; gb:zc78a07.s1 Pancreatic ist; ovar; diag
 125250; W26524; Hs.356686; protein phosphatase 4 regulator; ovar; CTL+s.m.
 125256; W90022; Hs.186809; ESTs; Highly similar to LCT2_H; angio; diag
 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
 125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 f; ovar; diag
 125770; AA143045; Hs.81668; v-kit Hardy-Zuckerman 4 feline; EWS; diag
 125976; AA436760; Hs.35552; gb:zu67011.r1 Soares_total_fet pros; diag
 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 60 126645; AA316181; Hs.61636; six transmembrane epithelial tr; pros, breast, lung, panc, headnk, EWS; mAb+CTL
 126768; AI559444; Hs.104679; ESTs; pros, breast; mAb
 126799; AW763865; Hs.74376; olfactomedin related ER locat; EWS; diag
 126872; AW450979; ; gb:UH-B13-ala-a-12-O-Uls1 N; blad; diag
 126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag
 126960; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.
 126968; R38438; Hs.118747; solute carrier family 15 (H+/p; pros; mAb
 127003; AW816515; Hs.1733640; ATPase, Class V, type 10D; pros; mAb
 127221; BE062109; Hs.241651; chloride channel, calcium act; lung, blad, headnk, cerv; mAb+s.m.
 127240; AJ05663; Hs.86998; nuclear factor of activated T; pros; CTL+s.m.
 75 127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb
 127478; D31152; Hs.179729; collagen, type X, alpha 1 (Sct; breast, lung, headnk, panc; diag
 127537; AI926047; Hs.162858; ESTs; pros; diag
 127664; AA806164; Hs.116502; ESTs; EWS; diag
 128046; AA873285; Hs.357313; gb:oh66805.s1 NCI_CGAP_Kid5 Ho; pros, breast, colon; diag
 128305; AI954568; Hs.365708; matrix Gla protein; breast; diag
 128478; AA708205; Hs.103043; ESTs; EWS; CTL+s.m.
 80 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

- 128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
 128734; AB008380; Hs.104570; kallikrein 8 (neuropsin/ovasin; ovar; diag
 128780; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, blad, panc; diag
 128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS; leuk; diag
 5 128854; BC159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
 128926; R67419; Hs.21851; Homo sapiens cDNA FLJ12900 fts; breast; diag
 128948; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
 128950; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, com; pros; diag
 10 129041; BE382756; Hs.169302; solute carrier family 2 (facit; lung, blad; mAb+s.m.
 129097; BE243933; Hs.108642; zinc finger protein 22 (KOX15; ovar; CTL+s.m.
 129098; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, blad, headnk; mAb+s.m.
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 129260; AF077200; Hs.279813; hypothetical protein; colon, diag
 129284; AA318224; Hs.296141; ESTs; colon; diag
 15 129352; U30246; Hs.110738; solute carrier family 12 (sodi; colon, breast, pros; mAb
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA; breast; diag
 129389; NM_012445; Hs.288126; spondin 2, extracellular matrix; colon, pros; diag
 129404; AI267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
 129466; L42683; Hs.334309; keratin 6A; lung, blad; diag
 20 129482; AA188195; Hs.289043; spindlin; breast; diag
 129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidemo; lung, blad, headnk; diag
 129620; D79338; CCR4-NOT transcription complex; breast, angio; diag
 25 129628; U36945; Hs.1174; cyclin-dependent kinase inhib; lung, blad, ovar, headnk; s.m.
 129650; AF109298; Hs.116258; prostate cancer associated pro; pros, EWS; diag
 129689; AW748482; Hs.77873; B7 homolog 3; breast; diag
 129703; BE380665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
 129869; AI222069; Hs.13015; hypothetical protein similar t; breast; diag
 129912; AF156096; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
 30 129953; AA412195; Hs.13740; ESTs; breast; diag
 129977; NM_000399; Hs.1395; early growth response 2 (Krox; EWS; CTL+s.m.
 130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag
 130057; AF027153; Hs.324767; solute carrier family 5 (inos; breast; mAb
 130095; AK001835; Hs.14933; hypothetical protein FLJ10773; breast; diag
 40 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 130181; AF052119; Hs.151608; Homo sapiens clone 23622 mRNA; pros; diag
 130184; HS83061; Hs.15166; retinoic acid induced 14; angio; diag
 130252; D63216; Hs.153894; frizzled-related protein; panc, EWS, stom, renal; diag
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
 45 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
 130385; AW057800; Hs.155223; stanniocalcin 2; breast, lung; mAb+diag
 130455; D90041; Hs.159966; N-acetyltransferase 1 (arylam); breast; s.m.
 130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag
 130558; BE564937; Hs.15984; pp21 homolog pros; CTL+s.m.
 130577; M69241; Hs.162; insulin-like growth factor b1n; ovar; diag
 50 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
 130637; AA356764; Hs.17109; integral membrane protein 2A; EWS; mAb+s.m.
 130648; AI458165; Hs.17296; hypothetical protein MGC2376; colon; diag
 55 130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.
 130690; AB006625; Hs.139033; paleomely expressed 3; ovar; diag
 130714; AJ348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
 130760; AW378130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 130800; AI187292; Hs.19574; hypothetical protein MGC5466; colon, lung; diag
 130839; AB011169; Hs.380675; similar to S. cerevisiae SSM4; angio; diag
 60 130844; U76249; Hs.20191; seven in absentia (Drosophila); breast; diag
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.
 130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 130957; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.
 65 130972; D61866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 130987; BE013269; Hs.21893; hypothetical protein DKFZp761N; colon; diag
 131046; AA321649; Hs.2246; small inducible cytokine subfz; breast, lung, blad, ovar, fibro; diag
 131080; NM_001955; Hs.2271; endothelin 1; angio; diag
 131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
 70 131148; AW553575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
 131216; AB154486; Hs.243901; Homo sapiens cDNA FLJ20738 fts; colon, breast; diag
 131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
 131244; AI638428; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
 75 131289; AA298696; Hs.333418; FXYD domain-containing ion tra; colon; diag
 131307; NM_000025; Hs.2549; adrenergic, beta-3, receptor; EWS; mAb
 131313; RS6290; Hs.76874; ribosomal protein L44; EWS; diag
 131492; AI452801; Hs.28869; nuclear receptor subfamily 2; pros; mAb+s.m.
 131544; AI355715; Hs.28655; programmed cell death 9 (PDCD9; breast; diag
 131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag
 80 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fts; breast; diag
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
 131643; AW410801; Hs.30026; HSPC182 protein; breast; diag
 131739; AFD017986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

131817; U20536; Hs.3280; caspase 6; apoptosis-related c; fibro, breast, cerv, lung, blad, panu, glio; s.m.
 131885; BE502341; Hs.3402; ESTs; breast; diag
 131919; T15803; Hs.272458; protein phosphatase 3 (former); pros, breast; s.m.
 131925; AF161048; Hs.183180; anaphase promoting complex sub; breast; diag
 5 131965; W79283; Hs.35962; ESTs; lung, ovar; diag
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, over; diag
 132050; AI267616; Hs.38022; ESTs; angio; diag
 132173; X88426; Hs.41718; endothelial cell-specific mole; angio; diag
 10 132180; NM_004602; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 f; ovar; diag
 132349; AW975564; Hs.181286; serine protease inhibitor, Kaz; pros, blad; s.m.
 132354; BE185289; Hs.1076; small proline-rich protein 1B; lung; diag
 132358; NM_002542; Hs.46428; H4 histone family, member G; pros; CTL+s.m.
 132371; AA235448; Hs.222084; PRO2000 protein; breast; diag
 15 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
 132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
 132520; AA257992; Hs.50851; Janus kinase 1 (a protein tyro; EWS; s.m.
 132528; T78738; Hs.50758; SMC4 (structural maintenance o; over; CTL+s.m.
 20 132543; BE558452; Hs.344037; protein regulator of cytokines; colon, lung; diag
 132572; AI929559; Hs.237828; signal recognition particle 72; ovar; diag
 132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22526 f; colon; diag
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
 132632; AU076916; Hs.5398; guanine monophosphate synthetase; ovar, lung; s.m.
 132669; W38680; Hs.380933; guanine nucleotide binding proc; colon; diag
 25 132710; W74001; Hs.55279; serine (or cysteine) proteinas; lung, blad, colon, headnk; diag
 132725; NM_006276; Hs.184167; splicing factor, argininosci; ovar; CTL+s.m.
 132787; BE182592; Hs.11251; small proline-rich protein 2A; lung; diag
 132791; AB029561; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
 132837; AA370362; Hs.57958; EGF-TM7-latrifilin-related pr; angio; diag
 30 132856; NM_001448; Hs.58357; glycan 4; breast, colon, pros; mAb
 132866; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
 132902; AI935442; Hs.59338; hypothetical protein FLJ10808; colon; diag
 132939; AB009284; Hs.61152; exostoses (multiple)-like 2; ovar; diag
 132984; AI362575; Hs.303171; ESTs; pros; diag
 35 132967; AA316181; Hs.61635; stx transmembrane epithelial a; pros, pros; mAb+CTL
 132990; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung; CTL+s.m.
 132994; AI112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
 133006; AW978436; Hs.62515; KIAA0494 gene product; colon; diag
 133016; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactose; breast, colon, pros; s.m.
 40 133018; AI439688; Hs.6289; hypothetical protein FLJ20886; breast; diag
 133051; AI186431; Hs.296638; prostate differentiation facto; angio, pros, blad; diag
 133063; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
 133070; U92494; Hs.380138; a disintegrin and metalloprote; leuk; diag
 133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 45 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
 133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 f; angio; diag
 133272; NM_002776; Hs.69423; kallikrein 10; colon, ovar; diag
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
 50 133321; T79526; Hs.179516; Integral type 1 protein; breast; diag
 133391; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag
 133415; X69699; Hs.73149; paired box gene 8; ovar; CTL
 133477; AW602335; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
 133579; X75348; Hs.75074; mitogen-activated protein kin; pros; diag
 133626; AW836130; Hs.75227; hypothetical protein FLJ13910; pros; diag
 55 133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb
 133829; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; over; diag
 133860; ST7298; Hs.76888; hypothetical protein MGC12702; blad; diag
 133944; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 60 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag
 133976; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
 134100; AA460086; Hs.171075; replication factor C (activato; pros; diag
 134110; U41060; Hs.79138; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
 134165; AI690916; Hs.178137; transducin of ERBB2, 1; breast; CTL+s.m.
 65 134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
 134318; BE304999; Hs.285764; fumurate hydratase; colon; s.m.
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
 134348; AW291946; Hs.82065; Interleukin 6 signal transduc; breast; mAb+s.m.
 134374; N22867; Hs.8236; ESTs; pros; diag
 70 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
 134401; AI916652; Hs.211577; kinase 1 (kinase receptor); pros, breast; mAb+s.m.
 134405; AW067903; Hs.82772; collagen, type XI, alpha 1; breast, lung, over, headnk; CTL
 134470; X64942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; over; s.m.
 75 134529; AW411479; Hs.848; FK506-binding protein 4 (53kD); breast; diag
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
 134654; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 134665; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
 134691; AW382987; Hs.88474; prostaglandin-endoperoxide syn; ovar; s.m.
 80 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
 134731; D69377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 134766; T28618; Hs.89640; TEK tyrosine kinase, endothel; angio; s.m.
 134824; S79723; Hs.298623; 5-hydroxytryptamine (serotonin; blad; mAb
 134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.

134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 134924; BE234029; Hs.279093; Ras homolog enriched in brain ; breast; mAb
 134972; AL033527; Hs.169252; v-myc avian myelocytomatisis v; ovary; CTL+s.m.
 134975; RS0333; Hs.92186; Lerman collet-cell protein; breast; diag
 5 134989; AW9568058; Hs.92381; nudix (nucleoside diphosphate : colon; diag
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 135117; W552493; Hs.94694; Homo sapiens cDNA FLJ10561 fis; breast; diag
 135166; AA135867; Hs.200858; ESTs; Highly similar to A35661; pros; diag
 135235; AW298244; Hs.286195; ESTs; angio; diag
 10 135242; AL553187; Hs.9700; cyclin E1; ovary; CTL+s.m.
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
 135255; Y13645; Hs.97234; iroplakin 2; blad; mAb
 135309; AL554123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag
 135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1670; pros; diag
 15 136389; U05237; Hs.99872; fetal Alzheimer antigen; pros; breast; colon; CTL+s.m.
 136400; X78592; Hs.9915; androgen receptor (dihydrotest; pros; mAb+s.m.
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros; breast; mAb+s.m.
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast; colon; lung; ovary; mAb+diag+s.m.
 20 300318; AW444502; Hs.256982; ESTs; Weakly similar to NEL1_H; angio; CTL+diag
 300605; AL218847; Hs.152670; ESTs; pros; diag
 300921; AF146747; Hs.232165; polycomb nubra vera 1; cel; pros; mAb+s.m.
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
 301042; AL859131; Hs.366053; hypothetical protein MGC2849; pros; mAb
 25 301043; AL160316; Hs.149155; voltage-dependent anion channel; pros; mAb+s.m.
 301050; AW136973; Hs.362915; ESTs; Weakly similar to S68890; colon; lung; CTL+s.m.
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast; lung; mAb+s.m.
 302001; AB020711; Hs.374965; KIAA0904 protein; breast ; CTL+s.m.
 302005; BE262922; Hs.123119; MAD (mothers against decapentap; pros; diag
 302057; BE542706; Hs.222399; CEGP1 protein; breast; diag
 302167; NM_006227; Hs.263007; phospholipid transfer protein; pros; mAb
 302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; pan); mAb+s.m.
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb+s.m.
 302290; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros; breast; diag
 35 302372; AL117405; Hs.335891; ATP-binding cassette transport; breast; pros ; mAb+s.m.
 302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast; cerv; diag
 302410; NM_004917; Hs.218366; kallikrein 4 (prostase; enamel; pros; diag
 302468; AL132561; Hs.380155; DKFZP434B081 protein; pros; diag
 302562; BE149762; Hs.48956; gap junction protein, beta 6 (-; lung; blad; mAb
 40 302881; AA509352; Hs.105314; relaxin 1 (H1); pros; diag
 303295; AA205625; Hs.200067; ESTs; blad; diag
 303380; AW952764; Hs.303171; olfactory receptor, family 51.; pros; mAb
 303506; AA340605; Hs.105887; ESTs; Weakly similar to Homolo; pros; breast; colon ; diag
 303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag
 45 303753; AW503733; Hs.9414; KIAA1488 protein; pros; breast; color; CTL+s.m.
 305503; AA759177; Hs.298148; ESTs; Weakly similar to KIAA05; pros; diag
 306273; AA836290 ; gbow70a01.1t Soares_NFL_T_GBC; pros; diag
 306676; AL005603 ; gbow15c10.1t NCI_CGAP_GC3 Horn; lung; diag
 306840; AN077477; Hs.307912; ESTs; angio; diag
 50 309177; AB51116; Hs.326738; Homo sapiens breast cancer ant; breast; pros; mAb+CTL
 309583; AW170035; Hs.328736; Homo sapiens breast cancer ant; breast; mAb+CTL
 309931; AW341683; Hs.343663; gb:hd13d01.1t Soares_NFL_T_GBC; lung; mAb
 310382; AT734009; Hs.127699; KIAA1603 protein; pros; diag
 310431; AI420227; Hs.360053; ESTs; Weakly similar to A46010; pros; diag
 55 310573; AW292180; Hs.156142; ESTs; pros; diag
 310636; AI814973; Hs.164175; ESTs; lung; diag
 310781; AI380797; Hs.158892; ESTs; breast ; diag
 310955; AI476732; Hs.263912; ESTs; breast; angio; diag
 311034; BE567130; Hs.311389; ESTs; Highly similar to NKGD_H; lung; mAb+s.m.
 60 311160; AB21005; Hs.118598; Intron of BPF9 (GDNFRa); breast ; diag
 311251; AI655662; Hs.197658; ESTs; pros; diag
 311657; AF200492; Hs.211236; interleukin-1 homolog 1; lung; diag
 311596; AJ682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 311630; AI915444; Hs.372037; ESTs; colon; blad; lung; ovar; panc; headnk; mAb+diag+s.m.
 311877; AA084249; Hs.372851; G protein-coupled receptor 39; ovar; angio; glio; mAb+s.m.
 65 311911; R19175; Hs.165793; ribosomal protein L32; pros; diag
 311926; T62216; Hs.378028; ESTs; pros; diag
 312182; T94344; Hs.326263; ESTs; pros; diag
 312252; AI128386; Hs.143856; ESTs; blad; diag
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
 312521; AI263307; Hs.356901; H2B histone family, member L; pros; breast; lung; diag
 70 312544; AA516420; Hs.352340; ESTs; Weakly similar to I38022; breast; diag
 312742; AI650363; Hs.116462; ESTs; colon; diag
 312795; AW975014; Hs.28; ferrocetelase (protoporphyrin pros; s.m.
 312857; BE083868; Hs.126914; KIAA1430 protein; colon; pros; CTL+s.m.
 312922; AA329268; Hs.378739; ESTs; Moderately similar to al; pros; diag
 313328; AW449211; Hs.105445; GDNFR family receptor alpha 1; breast ; mAb+s.m.
 313613; AW298600; Hs.64313; ESTs; Weakly similar to S59501; angio; mAb+s.m.
 313556; AA628517; Hs.118502; ESTs; angio; diag
 313665; AW751201; Hs.120932; ESTs; angio; diag
 80 313774; AI916059; Hs.144583; ESTs; colon; CTL
 313915; C18863; Hs.163443; intron of periosin (OSF-2αs); breast; diag
 313978; AI870175; Hs.13957; ESTs; angio; diag
 314078; AW129357; Hs.329700; ESTs; breast; diag

314097; AA648744; Hs.269493; ESTs; breast; diag
 314121; AI732083; Hs.187619; ESTs; pros, breast; diag
 314171; AI821895; Hs.193481; ESTs; pros; diag
 5 314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 f1; breast; diag
 314547; AA399272; Hs.144341; ESTs; breast; diag
 314558; AI873274; Hs.370280; ESTs; breast; pros; diag
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 f1; lung, blad; diag
 314591; AW207206; Hs.356982; ESTs; breast, pros; diag
 10 314765; AI38226; Hs.32976; guanine nucleotide binding pro; colon, pros; diag
 314907; AW971082; Hs.222886; ESTs, Weakly similar to TRH-Y_H; pros; diag
 315008; AI536613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 315033; AI493046; Hs.146133; ESTs; colon; diag
 15 315051; AW292425; Hs.163484; ESTs; colon; diag
 315052; AA876910; Hs.134427; ESTs; pros, breast; diag
 315198; AI367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
 315408; AW273261; Hs.216292; ESTs; pros; diag
 315534; AA837085; Hs.372254; ESTs; breast, pros; diag
 20 315720; AA292998; Hs.163900; ESTs; blad; diag
 316177; AI904982; Hs.283102; downstream of breast cancer an; breast; mAb+CTL
 316442; AA760894; Hs.125350; ESTs; pros; diag
 316580; AA938198; Hs.145123; poly(A) polymerase gamma; breast, angio; s.m.
 316886; AA035331; Hs.170261; ESTs; breast; diag
 25 316943; AW014875; Hs.137007; ESTs; blad; diag
 317078; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
 317140; AA085430; Hs.201925; Homo sapiens cDNA FLJ13446 f1; breast; diag
 317224; X73608; Hs.93029; sparcosinectin, cwcr and ka; pros; angio; diag
 317548; BE563568; Hs.159066; ESTs; pros; CTL+s.m.
 30 317803; AW684964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.
 317881; AI827246; Hs.224398; Homo sapiens cDNA FLJ11469 f1; breast, lung ; diag
 318240; AI085377; Hs.143610; ESTs; lung; diag
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros, colon; CTL+s.m.
 318532; AW139377; Hs.127179; cryptic gene; panc; diag
 35 318744; AI753124; Hs.144479; ESTs; breast; diag
 318754; W21423; Hs.44222; CG-90 protein; pros; diag
 319080; AW987646; Hs.23023; ESTs; pros; diag
 319795; AB037821; Hs.146558; probcadherin 10; pros, glo; mAb+s.m.
 320066; BE305242; Hs.16098; claudin 2; colon, panc; diag
 40 320157; AA984373; Hs.80790; Homo sapiens cDNA: FLJ22930 f1; breast, pros; diag
 320203; AL049227; Hs.124778; downstream of cadherin 6 (by 3; renal, ovar; mAb+s.m.
 320211; AL039402; Hs.125783; DEME-6 protein; breast, pros; CTL
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb
 320581; AF085808; Hs.159330; uropakin 3; pros; blad; diag
 45 320590; U67068; Hs.154299; Human proteinase activated rec; pros; mAb+s.m.
 320635; NS05617; Hs.88506; small nuclear ribonucleoprotein; angio lung; diag
 320798; AA315381; Hs.170195; bone morphogenetic protein 7 (f; ovar; mAb+diag
 320798; AK001641; Hs.31218; secretory carrier membrane pro; pros, colon ; diag
 50 320895; BE019924; Hs.271580; uropakin 1B; lung, blad, ovar, headnk; mAb+diag
 321023; AW294318; Hs.125608; ESTs; colon; diag
 321107; AI732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
 321412; AI674383; Hs.22891; solute carrier family 7 (galfr; pros; mAb+s.m.
 321441; AF107493; Hs.201676; Homo sapiens L1C4-15 protein nt; pros, breast; diag
 55 321644; AW975944; Hs.237395; ESTs; breast, pros; diag
 321717; AW956580; Hs.42698; ESTs; angio; diag
 321908; AW270608; Hs.170195; bone morphogenetic protein 7 (f; ovar; mAb+diag
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
 322035; AL137547; Hs.306201; hypothetical protein DKFZp564Q; breast, blad; mAb
 60 322521; AF147347 ; gb:Homo sapiens full length In; breast ; diag
 322705; AA018899; Hs.127179; cryptic gene; panc; diag
 322782; AA056080; Hs.202577; Homo sapiens cDNA FLJ12166 f1; pros; diag
 322818; AWD43782; Hs.293616; ESTs; pros, breast, angio, glo ; diag
 322882; AW248508; Hs.270727; Homo sapiens cDNA FLJ14035 f1; breast, lung, ovar, angio, blad; diag
 65 322975; C16391; intron of breast cancer antigen; breast ; mAb+CTL
 323188; AL120862; Hs.124165; programmed cell death 9 (FDD9; breast ; diag
 323226; AF055019; Hs.355279; Homo sapiens clone 24670 mRNA ; pros; diag
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 323287; AA635902; Hs.104215; ESTs, Moderately similar to SP⁺; pros; diag
 70 323332; AI829520 ; gb:W19c05x1 NCL_OGAP_Uti Hom; breast ; diag
 323335; AI655499; Hs.161712; ESTs; pros, breast; mAb
 323587; AI299709; Hs.131886; Homo sapiens cDNA: FLJ22113 f1; colon; diag
 323817; AA410943 ; NAME OMITTED .. receptor kinase; breast ; mAb
 75 324261; BE059341 ; gb:QV3-BT0381-270100-073-z08 B; breast; diag
 324295; AA434578; Hs.143891; ESTs; pros; diag
 324338; AA927668; Hs.145076; regulator of differentiation ; colon; diag
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 f1; pros, colon; diag
 324432; AA484510; Hs.152812; ESTs; breast, lung, panc; diag
 324603; AW993522; Hs.299887; ESTs; pros, breast; diag
 80 324617; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros; diag
 324658; AI694767; Hs.129179; Homo sapiens cDNA FLJ13681 f1; pros ; diag
 324718; AI557019; Hs.116467; small nuclear protein PRAC; colon, pros; diag
 324866; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
 324871; AI890347; Hs.271923; Homo sapiens cDNA: FLJ22785 f1; colon; diag

324987; AI375572; Hs.172634; E8Ts; breast; diag
 325372; Phase 2 & 3 Exons; breast; CTL+s.m.
 325544; Phase 2 & 3 Exons; breast; angio; diag
 5 327036; Phase 2 & 3 Exons; lung; angio; diag
 327075; Phase 2 & 3 Exons; breast, lung; diag
 327414; Phase 2 & 3 Exons; angio; diag
 328700; Phase 2 & 3 Exons; breast, angio; diag
 330211; Phase 2 & 3 Exons; pros; CTL+s.m.
 10 330468; L10343; protease inhibitor 3; skin-der; lung, colon, blad; diag
 330493; M27828; Hs.334372; endogenous retroviral protease; lung, colon; s.m.
 330630; NM_002802; Hs.79088; reductoculin 2; EF-hand calc; pros; diag
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
 330790; AI660243; Hs.318545; Hu01 Chir Redos; pros, blad; diag
 15 330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag
 330827; AI951486; Hs.249196; ESTs; lung, uter; diag
 330892; AF109298; Hs.118258; prostate cancer associated pros; pros; diag
 331014; AW770994; Hs.303440; hypothetical protein KIAA1165; colon; diag
 331151; R82331; Hs.121602; ESTs; pros, breast; diag
 20 331163; Y40769; Hs.8469; ESTs; colon; diag
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 f1; angio; diag
 331450; AF218751; Hs.26813; COA14; pros; diag
 331578; AI246402; Hs.243010; ESTs; angio; diag
 331614; N92293; Hs.208832; EST; Moderately similar to ALU; breast ; diag
 25 331811; AW885727; Hs.9914; Hu01 Chir Redos; lung; diag
 331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 331959; AA526911; Hs.827772; collagen type XI; alpha 1; breast, lung; CTL
 332180; AF134160; Hs.7327; claudin 1; lung; mAb
 332247; AA669097; ESTs; pros, breast; diag
 332396; AW579842; Hs.360730; hypothetical protein FLJ10897; pros; diag
 332453; L42583; Hs.334309; Hu01 Chir Redos; lung; diag
 332468; AB018259; Hs.118140; KIAA0716 gene product; angio; diag
 332530; M31669; Hs.1735; inhibin; beta B (activin AB be; ovar, pros; diag
 332553; AF167708; Hs.19280; cysteine-rich repeat-containln; angio; diag
 332840; BE568452; Hs.344037; protein regulator of cytokines; blad, headnk; diag
 332645; AA284371; Hs.118064; ESTs; breast, colon; diag
 332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.
 332897; X51405; Hs.75360; carboxypeptidase E; pros; diag
 332740; BE409669; Hs.286241; Homo sapiens cDNA: FLJ22698 f1; pros; diag
 40 332798; C22000007; gl[12314195]emb[CAB9; pros, breast ; diag
 333769; NM_005940; Homo sapiens matrix; breast, colon, lung; mAb+diag+s.m.
 333904; Chromosome 22; pros; diag
 334223; NM_005080; Homo sapiens X-box; pros, breast; diag
 334447; NM_012429; Homo sapiens SEC14; pros; diag
 45 335115; NM_008498; Homo sapiens lecfin; pros; CTL+s.m.
 335809; NM_014508; Homo sapiens krakon; breast; CTL+s.m.
 335824; ENSP00000249072; DJ222E13.1 (N; breast, pros; CTL+s.m.
 335825; ENSP00000249072; DJ222E13.1 (N; breast; diag
 335936; Chromosome 22; lung; diag
 50 336034; NM_007172; Homo sapiens nucleop; breast, angio; CTL+s.m.
 336152; NM_014242; homo sapiens cadher; breast ; mAb
 336636; C22000024; gl[10645308]glb[AAG2; lung, breast; CTL+s.m.
 338008; NM_005940; Homo sapiens matrix; lung, breast, colon; mAb+diag+s.m.
 338033; Chromosome 22; lung, angio; diag
 55 338158; NM_012399; Homo sapiens phosph; lung, angio; diag
 338255; NM_014323; Homo sapiens zinc t; pros, breast, colon ; CTL+s.m.
 400195; Hs.42650; NM_007057; Homo sapiens ZW10 t; lung; CTL+s.m.
 400289; Hs.253495; Eco Control; fibro; diag
 400285; Eco Control; lung; diag
 400287; S39329; Hs.181350; kallikrein 2, prostatic; pros; diag
 60 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin; panc, pros,angio, blad, lung; mAb+s.m.
 400290; H18896; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb
 400294; N95796; Hs.278695; Homo sapiens protein mRNA, cos pros, pros; mab
 400295; W72838; Hs.348419; AI905687; L-BT085-190199-019 B; breast; diag
 400298; AA032278; Hs.61635; six transmembrane epithelial s; panc, lung, headnk, stom, EWS, ovar; mAb+CTL
 65 400328; X87344; transporter 2, ATP-binding cas; lung; mAb+s.m.
 400409; AF153341; Homo sapiens winged helix/loc; blad; CTL+s.m.
 400419; AF084545; Target; lung, sarc; diag
 400440; X83957; Hs.83870; nebulin; sarc; diag
 70 400494; ENSP0000238970; CIG30 (Frame; angio; mAb
 400517; length; stom, cav, uter, lung, pros, colon, hepC; diag
 400651; ENSP0000228031; COPPER CHAPER; sarc; s.m.
 400685; NM_002425; Homo sapiens matrix ; lung; mAb+diag+s.m.
 400773; NM_003105; Homo sapiens sorbit bifid; mAb
 400844; NM_003105; Homo sapiens sorbit bifid; s.m.
 75 400846; sorbin-related receptor, LID; blad; mAb+s.m.
 400881; NM_025080; Homo sapiens hypoth; ovar; diag
 401093; C12000586; gl[6330167]objBA8; blad, lung; CTL+s.m.
 401234; mitogen-activated protein kinase; angio; diag
 80 401424; NM_001172; Homo sapiens arginas; pros; s.m.
 401468; C4000647; gl[4755508]refNP_00; headnk; mAb
 401704; NM_021195; Homo sapiens claud; test; mAb
 401732; NM_001176; Homo sapiens Rho GD; panc; diag
 401747; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, mela; diag

401760; ; Target Exon; blad, lung, headnk, esoph; diag
 401780; ; NM_005657:Homo sapiens kerat; lung, blad, headnk, esoph, mela; diag
 401781; ; Target Exon; lung, blad, headnk, esoph, cerv; diag
 401785; ; NM_002275:Homo sapiens kerat; lung; diag
 5 401797; ; Target Exon; sarc; diag
 401894; ; Target Exon; lung; diag
 402145; ; Target Exon; test; CTL+s.m.
 402199; ; Target Exon; test; CTL+s.m.
 10 402230; ; Fgenes3 predicted: CYTOCHROME ; blad; diag
 402239; ; Target Exon; blad; diag
 402260; ; NM_001438:Homo sapiens fibril; blad; CTL+s.m.
 402265; ; Target Exon; lung; diag
 15 402305; ; C19000735*:gi|4508027|ref|NP_0; blad; CTL+s.m.
 402420; ; C1000823*:gi|10432400|emb|CAC1; lung; diag
 402424; ; NM_024901:Homo sapiens hypoth; blad; CTL+s.m.
 402447; ; C1000201|gi|204416|gb|AAA02627; esoph; mAb
 402474; ; NM_004079:Homo sapiens catheps; lung, colon, stom, fibro; diag
 402550; ; Target Exon; fibro; diag
 402604; ; Target Exon; glio; diag
 20 402605; ; Target Exon; glio; diag
 402606; ; NM_024626:Homo sapiens hypoth; ovar, breast; mAb
 402580; ; Target Exon; test; mAb
 402777; ; C1002852*:gi|6444327|sp|Q04799; blad; diag
 402860; ; ENSP00000239210:DJ50024.4 (nov; mela; CTL+s.m.
 25 402888; ; Target Exon; sarc; diag
 402992; ; Target Exon; sarc; diag
 402994; ; NM_002463:Homo sapiens myxov; esoph; diag
 403046; ; NM_005656:Homo sapiens transm; pros; mAb
 30 403047; ; NM_005655:Homo sapiens transm; pros, blad, colon; mAb
 403071; ; NM_003319:Homo sapiens fibril; sarc; diag
 403088; ; NM_003319:Homo sapiens fibril; sarc; diag
 403171; ; C2001472*:gi|5809678|gb|AAB418; test; diag
 403226; ; Target Exon; mela; diag
 35 403329; ; unnamed protein product [Homo ; lung; diag
 403381; ; ENSP0000231844*:Ecotropic vir; blad; CTL+s.nt.
 403409; ; NM_005929:Homo sapiens antigen; mela; mAb
 403433; ; NM_001622:Homo sapiens alpha-2; hepC; diag
 403478; ; NM_022342:Homo sapiens kinesh; lung; CTL+s.m.
 403715; ; Target Exon; lung; diag
 403740; ; NM_001076:Homo sapiens UDP glc pros, hepC; s.m.
 403776; ; ENSP0000228542*:Small Induct; panc; diag
 403903; ; C6001632*:gi|10464308|gb|AAG21; blad; CTL+s.m.
 404029; ; NM_018936*:homo sapiens protoc; glio; mAb
 404049; ; NM_018937*:homo sapiens protoc; glio; mAb
 45 404210; ; NM_006936:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
 404240; ; NM_018950:Homo sapiens major h; fibro; mAb
 404253; ; NM_021058:Homo sapiens H2B h; lung; CTL+s.m.
 404286; ; C6001909|gi|704441|dbj|BA1890; panc; diag
 404298; ; C6001238*:gi|121715|sp|P26697; ; lung; s.m.
 50 404403; ; Target Exon; blad; diag
 404440; ; NM_021048:Homo sapiens melanom; lung, blad; mAb+CTL
 404866; ; ENSP0000251112*:Sodium/potass; panc; s.m.
 404877; ; NM_005365:Homo sapiens melanom; lung, blad; CTL+s.m.
 404927; ; Target Exon; lung, headnk; diag
 55 404996; ; Target Exon; lung, headnk, esoph; diag
 405001; ; interleukin enhancer binding f; sarc; diag
 405028; ; Homo sapiens bone morphogenet; angio; diag
 405121; ; mitogen-activated protein kin; angio, renat; s.m.
 405238; ; Target Exon; glio; diag
 60 405239; ; oxidative 3 alpha hydroxysterol; glio; s.m.
 405451; ; Homo sapiens glutaminyl-peptid; mela; mAb
 405545; ; Target Exon; cerv; mAb
 405546; ; NM_018833*:Homo sapiens transp; cerv; mAb
 65 405547; ; NM_018833*:Homo sapiens transp; cerv, mela; mAb
 405548; ; C12000290|gi|4557225|ref|NP_0; lung; diag
 406704; ; NM_001841*:Homo sapiens collag; sarc; diag
 405770; ; NM_002352:Homo sapiens melanom; lung, esoph; mAb+CTL
 405949; ; Target Exon; panc; diag
 70 405932; ; C15000305|gi|3806122|gb|AAC691; blad, lung, headnk, cerv; CTL+s.m.
 406081; ; Target Exon; blad; diag
 406137; ; NM_000179*:Homo sapiens muS (-; lung; CTL+s.m.
 406173; ; ENSP00000250148*:Growth hormon; panc; CTL+s.m.
 406348; ; Target Exon; breast; CTL+s.m.
 406360; ; Target Exon; lung, headnk; diag
 75 406399; ; NM_003122*:Homo sapiens serine; blad; diag
 406434; ; NM_030579*:Homo sapiens cytoch; blad; diag
 406467; ; Target Exon; lung, headnk, blad; diag
 406506; ; Target Exon; angio; diag
 406547; ; Target Exon; test; diag
 80 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
 406671; AA129547; Hs.285754; mel proto-oncogene (hepatocyte; panc; mAb
 406672; M26041; Hs.198253; major histocompatibility compl; fibro; mAb
 406686; M18728; gb; Human nonspecific crossreact; panc, colon, blad, headnk, stom, lung; mAb+CTL

406687; M31126; Hs.362054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
 406690; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
 5 406906; Z25424; ; gb:Human aspartic protein-serine/thr; blad, lung, s.m.
 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
 406987; M24349; ; gb:Human parathyroid hormone-t; lung; CTL+s.m.
 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
 10 407013; U356397; Hs.03870; gb:Human nebulin mRNA, partial; sarc; diag
 407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag
 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
 407118; AA156790; Hs.262036; ESTs; Weakly similar to Z223_4; pros; diag
 407122; H20276; Hs.31742; ESTs; pros; diag
 407137; T97307; ; gb:yee53h05.s1 Soares protein fib; lung, blad, ovar, pros, panc, headnk; diag
 15 407166; R45175; Hs.117182; ESTs; pros, breast, cerv; diag
 407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast; CTL+s.m.
 407202; N58172; Hs.109370; ESTs; pros; diag
 407216; N91773; Hs.348385; lysyl oxidase; panc; diag
 20 407242; M18728; ; gb:Human nonspecific crossreact; panc, colon, blad, headnk, stom, lung, over, cerv; mAb
 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
 407245; X90568; Hs.172004; titin; sarc; diag
 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
 407252; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
 25 407276; A185118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 ss; lung; diag
 407366; AF026942; Hs.17518; gb:Homo sapiens cig33 mRNA; pa; ovar, hepC, stom, mela, esoph; diag
 407581; R48402; Hs.173508; P3ECSL; blad; CTL+s.m.
 30 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
 407634; AW016569; Hs.138414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
 407710; AW022727; Hs.23616; ESTs; test; diag
 407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb
 407746; AK001982; Hs.38114; hypothetical protein FLJ11100; lung; diag
 35 407756; D80915; Hs.38385; KIAA0125 gene product; lung; diag
 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
 407782; AA608958; Hs.112819; ESTs; Moderately similar to PU; lung; diag
 407785; AA687538; Hs.38972; latrapsin 1; pros, colon, uter, stom, over, cerv; mAb
 407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
 407818; AL021938; Hs.40184; [uncon] (mouse) homolog; test; CTL+s.m.
 407824; AA147894; Hs.88112; Homo sapiens cDNA FLJ14388 ss; sarc; diag
 407839; AA045144; Hs.16166; ESTs; blad, headnk; mAb
 407846; AA262020; Hs.40403; Cbp/p300-interacting transact; mela; diag
 407853; AA336797; Hs.40498; dickkopf (Xenopus laevis) hornc; colon, stom, renal, breast, over, uter, cerv; diag
 45 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
 407872; AB039723; Hs.40735; fritzled (Drosophila) homolog; ovar; mAb
 407881; AW072003; Hs.40968; heparan sulfate (glucosamine); panc; s.m.
 407910; AA650274; Hs.41295; fibronectin leucine rich trans; fibro; mAb
 407944; R34008; Hs.239727; desmoclinin 2; lung, headnk, esoph; mAb
 50 407948; W21874; Hs.247057; ESTs; Weakly similar to 210926; fibro, blad; diag
 407952; AL139530; Hs.52930; ESTs; Weakly similar to S69501; angio; mAb+s.m.
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (s; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
 55 408045; AW138859; Hs.245123; ESTs; breast; diag
 408056; AA312329; Hs.42331; ephrin-A4; over; diag
 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
 408081; AW451597; Hs.167409; Intron of basic-helix-loop-hel; ovar; glio; diag
 408101; AW968504; Hs.278348; CDC2-related protein kinase 7; breast, lung, stom; s.m.
 60 408122; A1432652; Hs.42824; hypothetical protein FLJ10718; lung; diag
 408209; NM_004454; Hs.43697; ests variant gene 5 (ets-relate; mela; CTL+s.m.
 408298; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0; panc, renal, colon; mAb
 408353; BE439838; Hs.44298; mitochondrial ribosomal protein; lung; diag
 408430; S79876; Hs.44928; dipeptidylpeptidase IV (CD26; ; pros; mAb
 65 408522; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, esoph, cerv; diag
 408561; AA525775; Hs.89040; ESTs; Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
 408570; AL046408; Hs.103463; KIAA1798 protein; angio; CTL+s.m.
 408572; AA055811; Hs.226568; ESTs; Moderately similar to AL; lung; diag
 70 408591; AP015224; Hs.46452; mammaglobin 1; breast, cerv; diag
 408611; NM_004367; Hs.45468; chemokine (C-C motif) receptor; mela; mAb
 408633; AW963372; Hs.222088; PRO2000 protein blad, lung, headnk, pros; diag
 408660; AA525775; Hs.89040; ESTs; Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
 408728; AL137378; Hs.47125; hypothetical protein FLJ13912; test; diag
 408768; NM_003680; Hs.47504; exonuclease 1; mela; CTL+s.m.
 75 408770; AW270808; Hs.170195; bone morphogenetic protein 7; over; mAb+diag
 408771; AW732573; Hs.47504; potassium voltage-gated channel; lung; mAb
 408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag
 408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag
 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
 80 408833; AW612232; Hs.254635; ESTs; pros; diag
 408877; AA479033; Hs.130315; ESTs; Weakly similar to A47582; breast; diag
 408915; NM_016851; Hs.46950; hepatocellular carcinoma novel ; panc, sarc; diag
 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

408962; BE398436; Hs.44317; SRY (sex determining region Y); mela; diag
 408992; AA059325; Hs.30114; guanine nucleotide binding pro; fung; diag
 408996; AF979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.
 5 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.
 409038; T97490; Hs.50002; small inducible cytokine subf; mela; diag
 409051; AA080912; gb2n04d03_r1 Stratagene hNT n; pros; s.m.
 409077; AA063037; Hs.66803; ESTs; lung; diag
 409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
 10 409123; AA063403; gb2m04d12_s1 Stratagene come; pros; s.m.
 409142; AL136877; Hs.50758; SMC4 (structural maintenance o; over, lung, mela; diag
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
 409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.
 409228; R16811; Hs.22010; ESTs; Weakly similar to 210926; lung; mAb
 15 409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros; over, breast, uter, panc, colon, stom; mAb
 409243; AB037761; Hs.51743; KIAA1340 protein; test; diag
 409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
 409284; NM_014937; Hs.52463; KIAA0966 protein; mela; CTL+s.m.
 20 409289; AA578953; Hs.22972; sterol 5 alpha-reductase 2-ii; breast, ovar, lung, panc, uter; mAb
 409327; L41162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; mela; CTL+s.m.
 409342; AJ077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
 409348; AJ015356; Hs.146090; ESTs; renal, gllo; diag
 409361; NM_005982; Hs.54416; sine oculis homeobox (Drosophila); blad, lung, pros; CTL+s.m.
 409369; AB007979; Hs.301281; Homo sapiens mRNA, chromosome 1; gllo; diag
 409395; U46745; Hs.338678; dystrobrevin, alpha; gllo; diag
 409402; AF209234; Hs.655; cystatin B (stefin B); blad; diag
 409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 f1; mela; diag
 409421; AA199883; Hs.87624; ESTs; test; diag
 30 409430; R21945; Hs.346735; splicing factor, arginine/sari; mela; diag
 409432; D49372; Hs.54460; small inducible cytokine subf; stom, esoph; diag
 409433; AA074382; Hs.135255; ESTs; gllo; sarc; diag
 409509; AL036923; Hs.322710; ESTs; emgor; diag
 409512; AW979187; Hs.2933591; melanoma differentiation assoc; mela, esoph; CTL+s.m.
 35 409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 409562; R27430; Hs.271565; ESTs; lung; diag
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.
 409639; AW449822; Hs.55200; ESTs; sarc; diag
 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag
 409638; AW450420; Hs.21338; ESTs; gllo; diag
 409670; AI368109; Hs.3B1163; KIAA1856 protein; test; CTL+s.m.
 409703; NM_006187; Hs.580103; 2'-5'-oligoadenylate synthetase; panc, esoph, mela; s.m.
 409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
 45 409719; AI769160; Hs.106881; Homo sapiens brain tumor assoc; lung; diag
 409731; AA125985; Hs.56145; thyrosin, beta, identified in ; pros, sarc; CTL+s.m.
 409745; AA077391; gb:7B14E12 Chromosome 7 Fetal ; ovar, renal; CTL+s.m.
 409936; AW511413; Hs.167393; ESTs; lung; diag
 409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
 409988; N27657; Hs.334334; transcription factor AP-2 alph; mela; diag
 50 410006; AW732308; Hs.57783; eukaryotic translation initiat; test; diag
 410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
 410044; BE566742; Hs.58169; highly expressed in cancer, ri; blad; diag
 410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.
 55 410076; T05987; Hs.7991; ESTs; lung, pros; diag
 410079; U94362; Hs.380757; glycogenin 2; mela; diag
 410082; AA081594; Hs.158311; Murashii (Drosophila) homolog 1; pros; diag
 410102; AW248508; Hs.279727; ESTs; homologue of PEM-3 [Cion]; over, breast, blad, lung, anglo, sarc; diag
 410174; AA306807; Hs.58461; DKFZP434C246 protein; mela; diag
 410240; AI157424; Hs.61289; synaptophysin 2; angio; diag
 60 410247; AF181721; Hs.61345; RU28; ovar; CTL+s.m.
 410268; AA316181; Hs.61635; sbx transmembrane epithelial a; panc, pros, EWS; mAb+CTL
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag
 410310; JG2931; Hs.62192; coagulation factor III (thromb); pros, panc; mAb
 410361; BE391804; Hs.62661; guanylate binding protein 1, i; mela, esoph, hepC, fibro, uter; diag
 410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
 65 410457; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
 410480; R57457; Hs.63984; cadherin 13, H-cadherin (heart; anglo; mAb
 410491; AA465131; Hs.64001; Homo sapiens clone 26218 mRNA ; mela, esoph; diag
 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; over; mAb
 70 410553; AW016824; Hs.272058; hypothetical protein MGC14128; blad, lung; diag
 410555; UB2849; Hs.380135; a disintegrin and metalloprotein; leuk, lung; mAb
 410561; BE540255; Hs.6394; Homo sapiens cDNA: FLJ22044 f1; lung; diag
 410566; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 f1s; panc; diag
 410600; AW575742; Hs.351676; ESTs; Moderately similar to S6; mela; mAb+s.m.
 75 410621; AA194329; Hs.172004; tian; sarc; diag
 410681; AW246890; Hs.65425; cathepsin 1, (28kD); lung; diag
 410687; U24388; Hs.66436; lysyl oxidase-like 1; panc; diag
 410733; D84284; Hs.660852; CD38 antigen (p45); pros; mAb+CTL
 410763; AF279145; Hs.8965; hypothetical protein FLJ21776; panc; mAb
 80 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
 410857; X63598; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
 410870; UB1599; Hs.66731; homeo box B13; pros; CTL+s.m.
 410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1); leuk; diag

- 410869; X91662; Hs.66744; twist (*Drosophila*) homolog (sc; ssrC; CTL+s.m.
 410929; H47233; Hs.30643; ESTs; ovar; test; diag
 411076; AI222020; Hs.182364; CocoCrisp; pros, glo, breast; diag
 411089; AA456454; Hs.214291; cell division cycle 2-like 1 ; lung, fibro; CTL+s.m.
 5 411243; AB030986; Hs.69319; CA11; esoph; diag
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fs; blad; diag
 411257; AA628967; Hs.115274; Indian hedgehog protein (IHH) ; ovar; diag
 411263; BE297802; Hs.89360; kinesin-like 6 (mitotic centri; lung, blad, headnk; CTL+s.m.
 10 411266; BE207307; Hs.10114; growth suppressor 1; sanc; diag
 411358; R47479; Hs.94761; KIAA1691 protein; mela,renal, sanc; mAb
 411388; X72925; Hs.69752; desmocollin 1; headnk, mela; mAb
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMENT); ovar; diag
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) ; panc, pros, stom, breast, uter, cerv, ovar; mAb
 15 411573; AB029000; Hs.70823; KIAA1077 protein; panc, headnk, lung, stom; diag
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
 411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag
 411768; NM_013371; Hs.71879; Interleukin 19; ovar, uter, cerv; diag
 411789; AF-245505; Hs.72157; Adican; breast, panc, lung, stom, headnk, ovar, uter, esoph, sanc; diag
 20 411825; AK000334; Hs.352415; solute carrier family 39 (zinc); colon, ovar; mAb
 411826; AW181449; Hs.72290; wingless-type MMTV Integration; ovar; diag
 411869; W20027; Hs.23439; ESTs; anglo; diag
 411874; AA096106; Hs.20403; ESTs; blad; diag
 411880; AW872477; glcm30103.x1 NCI_CGAP_Thy4 Ho; blad; diag
 25 411945; AL033527; Hs.92137; L-myo-2 protein (MYCL2); blad, ovar; CTL+s.m.
 412006; AW451618; Hs.380683; ESTs; sanc; diag
 412026; AA383618; Hs.73073; testis-specific ankyrin motif ; test; diag
 412045; AA098802; Hs.83883; transmembrane, prostate androg; pros; mAb+s.m.
 412099; U64198; Hs.73165; Interleukin 12 receptor, beta ; leuk, mela; mAb
 30 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc, fibro; diag
 412116; AK001763; Hs.73239; hypothetical protein FLJ10901; lung, blad; CTL+s.m.
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
 412133; U83460; Hs.380728; solute carrier family 31 (copper); pros; mAb
 412226; AW503785; Hs.73792; complement component 3d/Epsite; mela; mAb
 412247; AF-022375; Hs.73753; vascular endothelial growth fa; renal, glo, blad, color; diag
 35 412265; AA101325; Hs.88154; hypothetical protein FLJ12457; test; CTL+s.m.
 412326; R07566; Hs.73817; small inducible cytokine A3 (h); pros, leuk; diag
 412351; AA135960; Hs.73826; T-cell acute lymphocytic leuke; angio; CTL+s.m.
 412420; AL035868; Hs.73853; bone morphogenetic protein 2; blad, glo, lung, stom, angio; diag
 40 412448; L12984; Hs.73895; tumor necrosis factor receptor; leuk; mAb
 412471; MS3193; Hs.73946; endothelial cell growth factor; cerv, mela, esoph; diag
 412490; AW803584; Hs.288850; Homo sapiens cDNA: FLJ22528 f1; mela; diag
 412519; AA196241; Hs.73980; tropomod T1, skeletal, slow; sanc; diag
 412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad, lung; diag
 45 412684; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
 412580; AA113262; Hs.17901; similar to CABLES [Homo sapien]; mela; diag
 412610; X90908; Hs.74126; fatty acid binding protein 6 ; blad; diag
 412661; N32860; Hs.24611; ESTs; Weakly similar to I54374; blad; CTL+s.m.
 50 412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
 412723; AA648469; Hs.335951; hypothetical protein AF301222; lung, blad, headnk, colon, stom, uter; diag
 412755; BE144306; Hs.179891; ESTs; Weakly similar to P4fIA_H; anglo; s.m.
 412811; H06382; Hs.349705; ESTs; lung; diag
 412817; AL037158; Hs.74819; proteasome (prosome, macropain; lung; s.m.
 412843; AF007655; Hs.74624; protein tyrosine phosphatase; pros; mAb
 55 412856; BE396745; Hs.74631; basigin (OK blood group); mela; mAb
 412926; AB79078; Hs.75061; macrophage myristoylated alant; mela; CTL+s.m.
 412939; AW411491; Hs.75068; eukaryotic translation elongat; mela, renal; diag
 412970; AB026428; Hs.177534; dual specificity phosphatase 1; breast, mela; s.m.
 412995; X81120; Hs.75110; cannabinoid receptor 1 (brain); glo; mAb
 60 413004; T35901; Hs.76117; interleukin enhancer binding f; lung; diag
 413011; AW088115; Hs.821; blgycan; lung; CTL+s.m.
 413049; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
 413095; AA494359; Hs.30715; potassium voltage-gated channel; panc, stom, renal, colon; mAb+s.m.
 413126; BE244589; Hs.75207; glyoxalase 1; pros; s.m.
 65 413126; AW419203; Hs.174174; ESTs; anglo; diag
 413129; AF292100; Hs.104613; RP42 homolog; lung; diag
 413132; NM_008823; Hs.75209; protein kinase (cAMP-dependent; anglo; CTL+s.m.
 413142; MB1740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
 70 413163; Y00816; Hs.75218; protein tyrosine phosphatase; pros; mAb
 413171; AA318325; Hs.75219; tyrosine-related protein 1; mela; mAb
 413190; AA151802; Hs.40368; adaptor-related protein comple; mela; diag
 413219; AA876200; Hs.118727; Homo sapiens cDNA FLJ13892 fs; esoph, cerv;
 413223; AI732182; Hs.191866; ESTs; lung; diag
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.
 75 413281; AA861271; Hs.222024; transcription factor SMAL2; lung, blad, headnk, panc, angio; diag
 413313; NM_002047; Hs.29386; glycol-tRNA synthetase; test; s.m.
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble; pros; s.m.
 413338; AB131318; Hs.48442; ESTs; ovar; diag
 413364; BE536218; Hs.137516; filgelin-like 1; lung; diag
 413372; H55532; Hs.349695; tubulin, alpha 2; test; diag
 80 413435; X51405; Hs.75360; carboxypeptidase E; pros, glo, panc, sanc; diag
 413436; AF236083; Hs.68061; sphingosine kinase 1; sanc; s.m.
 413472; BE242870; Hs.75379; solute carrier family 1 (glut; glo); mAb
 413566; AW604451; Hs.381153; sprouty (*Drosophila*) homolog 4; sanc; CTL+s.m.

413573; AI733859; Hs.149089; ESTs; lung; diag
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
 413597; AW302685; Hs.117183; ESTs; pros; diag
 5 413623; AA825721; Hs.246973; intron of Bicaudal D homolog 1; ovar, pros; diag
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
 413711; AW291765; Hs.75486; heat shock transcription factor; renal; diag
 413753; U17760; Hs.75617; laminin, beta 3 (niclin) (125kD); lung, blad, headnk, panc, carv, esoph, colon; diag
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
 413778; AA090235; Hs.75535; myosin light polypeptide 2, r; sarc; diag
 10 413794; AF234532; Hs.61638; myosin X; mele; diag
 413804; T64682; gbyc48102.1; Strategen; liver; blad; diag
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesme; esoph; diag
 413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag
 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
 15 413842; M29383; Hs.856; Interferon, gamma; leuk; diag
 413859; NM_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb
 413880; AI650842; Hs.110915; Interleukin 22 receptor; panc, colon; mAb+s.m.
 413924; AL119984; Hs.75618; seladin-1; pros, breast, ovar; diag
 20 413943; AW294416; Hs.144887; Homo sapiens cDNA FLJ12981 fis; blad, lung; CTL+s.m.
 413985; AI018666; Hs.75687; synaptophysin; gllo, sarc; mAb
 414004; AA737033; Hs.7155; ESTs; Moderately similar to 21; panc, mele; diag
 414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
 414034; UB9277; Hs.305985; early development regulator 1; test; CTL+s.m.
 25 414035; Y00630; Hs.75716; serine (or threonine) protein; lung, carv, headnk, blad; s.m.
 414053; BE391638; Hs.75725; transglutin 2; blad; diag
 414061; NM_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 fis; pros; diag
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 family; pros, panc, sarc; s.m.
 30 414142; AW368397; Hs.334485; hemilentin (lulin 6); fibro, panc, sarc; diag
 414161; AA136106; Hs.184852; KIAA1553 protein; test; diag
 414166; AW888941; Hs.75789; N-myct downstream regulated; pros, renal; diag
 414217; AJ309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis; glic; diag
 414219; W20010; Hs.75823; ALL1-fused gene from chromosome; sarc; diag
 414221; AW450979; gbt:U1-H-B13-ala-a-12-O-U1-N; blad; diag
 35 414251; AL042305; Hs.97688; VASA protein; test; CTL+s.m.
 414259; W44633; Hs.301298; Integrin, beta-like 1 (with EG; panc; diag
 414334; AA624298; Hs.21331; hypothetical protein FLJ10036; test; diag
 414359; M62194; Hs.75925; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
 40 414368; W70717; Hs.75939; uridine monophosphate kinase; lung; s.m.
 414386; X00442; Hs.75990; haptoglobin; ovar; diag
 414416; AW409895; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
 414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag
 414424; AJ348201; Hs.78118; ubiquitin carboxyl-terminal est; lung; s.m.
 45 414443; AU077288; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 414477; U41835; Hs.76228; amplified in osteosarcoma; sarc; diag
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); mele; mAb
 50 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colm, stom, fibr; diag
 414565; AA510297; Hs.183390; hypothetical protein FLJ13590; pros; diag
 414569; AF109288; Hs.118258; prostate cancer associated pros; pros, EWS; diag
 414576; H11257; Hs.375743; Homo sapiens clone IMAGE45183; renal; diag
 55 414595; AA641728; Hs.289015; hypothetical protein MGC4171; blad; diag
 414602; AW630086; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
 414683; S78296; Hs.76988; hypothetical protein MGC12702; blad, lung, test; diag
 414732; AW410976; Hs.77152; minichromosome maintenance def; test; blad; diag
 414761; AU077228; Hs.77256; enhancer of zeste (*Drosophila*); lung, blad, test; CTL+s.m.
 60 414776; AA155599; Hs.212833; hypothetical protein FLJ14185; angio; diag
 414786; AI246482; Hs.243010; Homo sapiens cDNA FLJ14372 fis; angio; diag
 414795; AI762416; Hs.77326; insulin-like growth factor b1; renal; diag
 414806; D14894; Hs.77329; phosphatidylserine synthase 1; lung; mAb
 414807; AI738816; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.
 414809; AM34569; Hs.77356; transferrin receptor (p90, CD7); lung; mAb+s.m.
 65 414825; X06370; Hs.77432; epidermal growth factor recep; gllo, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.
 414919; NM_002462; Hs.763391; myxovirus (influenza) resistant; esoph; diag
 414918; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 70 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
 414945; BE076358; Hs.77687; lymphocyte antigen 6 complex; mele; mAb
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
 414998; NM_002543; Hs.77729; oxidized low density lipopote; fibro, ovar, panc, colon; mAb
 415003; M11437; Hs.77741; Kininogen; panc; diag
 415025; AW207091; Hs.72307; ESTs; blad; diag
 415091; AI044872; Hs.77910; 3-hydroxy-3-methylglutaryl-CoA; lung, headnk; s.m.
 75 415178; D80503; Hs.48692; ESTs; blad; diag
 415214; AI445236; Hs.125124; EphB2; colon, stom; mAb
 415314; N88802; Hs.5422; glycoprotein M6B; mele; mAb
 415457; AW081710; Hs.73682; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.
 415511; AI732617; Hs.182362; ESTs; blad, ovar, renal; diag
 415542; R13474; Hs.290263; ESTs; Weakly similar to 138022; blad; diag
 80 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
 415752; BE514524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, mele; mAb
 415786; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 415787; H01463; Hs.93534; ESTs; pros; diag
 415819; AU077330; Hs.360791; transcription elongation facto; test; CTL+s.m.

- 415829; AW450198; Hs.163742; ESTs; test; diag
 415857; AA866115; Hs.127787; Homo sapiens cDNA FLJ11381 fts; lung; test; diag
 415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
 415947; U04045; Hs.78934; mutS (*E. coli*) homolog 2 (colo; test; diag
 5 415980; AI267700; Hs.351201; ESTs; pros; ovar; blad; lung; headnk; panc; colon; sarc; diag
 415992; CO5837; Hs.145807; hypothetical protein FLJ13593; pros; fibro; mAb
 415999; AA172179; Hs.294029; ESTs; pros; uter; diag
 416016; AW138239; Hs.78977; proprotein convertase subtilis; colon; panc; lung; diag
 416030; H15261; Hs.21948; ESTs; breast; fibro; diag
 10 416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad; lung; headnk; mela; CTL+s.m.
 416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung; stom; CTL+s.m.
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
 416201; AA487752; Hs.195161; ESTs; test; diag
 15 416208; AW291168; Hs.41295; ESTs; Weakly similar to MUC2_H; lung; diag
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag
 416225; AA577730; Hs.188684; ESTs; Weakly similar to PC4265; pros; blad; diag
 416350; AF188628; Hs.189507; phospholipase A2, group II; test; mela; fibro; diag
 416370; N90470; Hs.203697; CD38 antigen (p45); pros; glio; mAb+CTL
 20 416373; AA195845; Hs.73680; ESTs; Weakly similar to S12658; sarc; diag
 416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
 416448; L13210; Hs.79339; lectin galactoside-binding, s; ovar; colon; stom; diag
 416498; U33632; Hs.79351; potassium channel, subfamily K; panc; stom; breast; ovar; colon; mAb
 416539; Y07909; Hs.79368; epithelial membrane protein 1; pros; headnk; diag
 25 416602; NM_005159; Hs.357695; Protein kinase C-binding protein; breast; diag
 416840; BE262478; Hs.13408; neuron-specific protein; mela; diag
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad; lung; headnk; cerv; panc; anglo; diag
 416773; AK000340; Hs.79828; hypothetical protein FLJ120333; test; CTL+s.m.
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactose; anglo; s.m.
 30 416819; U77735; Hs.80205; pim-2 oncogene; lung; test; diag
 416881; N32620; Hs.141358; ESTs; mela; diag
 416929; N20635; Hs.43265; metastatin 1; mela; diag
 416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytoto; mela; s.m.
 417003; AL038170; Hs.80758; betaine-homocysteine methyltria; blad; s.m.
 417070; Z19077; Hs.172004; fib; sarc; diag
 35 417105; X600992; Hs.81226; CD6 antigen; fibro; mAb
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein; test; CTL+s.m.
 417124; BE122762; Hs.25338; ESTs; angio; diag
 417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag
 417151; AA194055; Hs.293858; ESTs; blad; diag
 40 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros; sarc; diag
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
 417237; H86386; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
 417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc; breast; diag
 45 417275; X63578; Hs.295449; parvalbumin; blad; diag
 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
 417308; H60720; Hs.81892; KIAA0101 gene product; lung; headnk; blad; cerv; anglo; mela; ear; diag
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
 417333; AL157545; Hs.173179; bromodomain and PHD finger com; breast; diag
 417355; D13168; Hs.82002; endothelin receptor type B; glio; mela; mAb
 417365; D50683; Hs.82028; transforming growth factor, beta; fibro; anglo; mAb
 45 417366; BE185289; Hs.1076; small proline-rich protein 1B; lung; blad; headnk; panc; esoph; mela; diag
 417370; T26551; Hs.374468; tryptophanyl-tRNA synthetase; fibro; mela; diag
 417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 50 417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 417407; AA923278; Hs.290805; ESTs; Weakly similar to protea; test; pros; s.m.
 417409; BE272506; Hs.82193; syndecan 1; blad; diag
 417412; X16896; Hs.82112; Interleukin 1 receptor, type I; fibro; pros; panc; mAb
 417426; NM_002291; Hs.82124; laminin, beta 1; angio; diag
 417437; US2682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
 55 417512; X76534; Hs.82228; glycoprotein (transmembrane) n; lung; mela; headnk; panc; breast; mAb
 417515; L24203; Hs.82237; aldo-keto-reductase family D; lung; headnk; blad; diag
 417542; J04129; Hs.82269; progestagen-associated endomet; lung; mela; diag
 417592; AA204684; Hs.182437; ESTs; Weakly similar to 154383; test; diag
 417599; AA204688; Hs.62964; ESTs; blad; esoph; diag
 60 417621; AV654694; Hs.82316; interferon-induced, heparin; esoph; diag
 417696; BE241624; Hs.82401; CD89 antigen (p60, early T-cell; pros; mAb
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
 417715; AW969587; Hs.86386; ESTs; blad; lung; headnk; diag
 417720; AA205625; Hs.208067; ESTs; blad; lung; esoph; headnk; diag
 417750; AI267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
 417777; AI823763; Hs.7055; ESTs; Weakly similar to 178885; test; s.m.
 70 417791; AW956339; Hs.44269; ESTs; ovar; blad; lung; headnk; CTL+s.m.
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc; fibro; diag
 417805; U38545; Hs.82587; phospholipase D1, phosphatidyl; anglo; s.m.
 417831; H16423; Hs.82685; CD47 antigen (Rh-related antig; ovar; mAb
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fts; pros; diag
 417847; AI521650; Hs.7331; hypothetical protein FLJ22316; ovar; diag
 417849; AW291587; Hs.82733; nidogen 2; anglo; headnk; diag
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, ; panc; mAb+s.m.
 75 417880; BE241595; Hs.82848; selectin_L (lymphocyte adhesio; mela; mAb
 417886; AA214584; ESTs; test; ovar; diag
 417900; BE250127; Hs.82908; CDC20 (cell division cycle 20; lung; stom; test; blad; headnk; cerv; esoph; CTL+s.m.
 417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

- 417944; AU077196; Hs.82986; collagen, type V, alpha 2; sarc; diag
 417975; AA641836; Hs.30085; hypothetical protein FLJ23188; colon, stom, lung; mAb
 417976; BE665892; Hs.83077; interleukin 1B (interferon-gam); colon, stom, fibros; diag
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 fam1; lung, headnk, esoph; s.m.
 5 418036; Z37976; Hs.83337; latent transforming growth fac; angio; diag
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
 418067; AI127958; Hs.83393; cyclin EM; headnk, panc, blad; diag
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUESS; blad; s.m.
 10 418113; AI272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glo, test, sarc; CTL+s.m.
 418134; AA397769; Hs.86617; ESTs; test; diag
 418140; BE513836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
 418156; WI17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
 15 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
 418216; AA662240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag
 418245; AA080767; Hs.83683; transmembrane, prostate androg; panc; mAb+s.m.
 418283; S79895; Hs.83942; cathepsin K (pachnodystosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhib; headnk, lung, blad; s.m.
 20 418336; NM_002522; Hs.84154; neuronal pentraxin 1; sarc; diag
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinas; cerv, lung; s.m.
 418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb
 418379; AA218940; Hs.137516; fibrinogen-like 1; lung; diag
 25 418394; AF132818; Hs.84720; Kruppel-like factor 5 (intest; panc; CTL+s.m.
 418396; AI765805; Hs.26691; SLC2A12 Solute carrier family; pros; mAb
 418397; NM_001269; Hs.84746; chromosome condensation 1; lung; diag
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
 418406; X73501; Hs.84905; cyclokerafin 20; blad, colon; diag
 30 418432; M14156; Hs.85112; insulin-like growth factor 1 (pros, fibro; diag
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide fibro; mAb
 418462; BE001596; Hs.85268; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
 418543; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb
 418576; AW968158; Hs.302740; epithelial calcium channel 2; pros; mAb+s.m.
 35 418610; AW245893; Hs.32417; hypothetical protein MGC2742; pros; diag
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
 418655; AA228354; Hs.111240; ESTs; pros; diag
 418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
 40 418663; AK001100; Hs.41890; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
 418683; US9098; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.
 418686; Z36930; Hs.87268; amuskin AB; blad, lung; diag
 418693; AI760876; Hs.87409; thrombospondin 1; angio, panc; diag
 418696; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag
 418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag
 418766; AA252254; Hs.228949; ESTs; test; diag
 45 418825; AA220881; Hs.22384; hypothetical protein FLJ10893; angio; diag
 418829; AA516531; Hs.65993; Nr homeobox (Drosophila); tam; pros; diag
 418832; NM_004996; Hs.89433; ATP-binding cassette, sub-fam1; ovar, pros, breast, lung; diag
 418833; BE387036; Hs.1211; acid phosphatase 5, testicul r; fibro; s.m.
 50 418886; AU076801; Hs.89436; cadherin 17, LI cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.
 418918; X07871; Hs.89476; CD2 antigen (p50); sheep red b; mela, fibro; mAb
 418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glo; mAb
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
 418956; NM_000078; Hs.89530; cholestenol ester transfer pro; mela; diag
 55 418994; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, angio; mAb
 419038; AW134942; Hs.68220; ESTs; pros; diag
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2 ; ovar, renal, blad, lung; mAb
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
 60 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
 419092; J05581; Hs.99603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
 419222; AD001520; Hs.89718; spermine synthase; pros; s.m.
 419223; X60111; Hs.1244; CD8 antigen (p24); breast, pros, ovar; mAb
 419231; AL046294; Hs.135245; ESTs, Weakly similar to T17227; fibro; diag
 65 419251; X07876; Hs.89791; wingless-type MMTV integration; panc; diag
 419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB_B; pros; diag
 419280; AI129114; Hs.112888; spinal cord-derived growth fac; panc; diag
 419356; AI656168; Hs.7331; hypothetical protein FLJ22316; uter, ovar, diag
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
 70 419440; AB020889; Hs.80410; KIAA0882 protein; breast; diag
 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytoto; fibro; s.m.
 419519; AI198719; Hs.176370; ESTs; mela; diag
 419551; AW582256; Hs.91011; anterior gradient 2 (Xenopus); panc, pros, breast; diag
 419559; Y07826; Hs.91098; ring finger protein; blad, colon, stom; CTL+s.m.
 75 419568; AB026116; Hs.263078; hQAT4; renal; mAb
 419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
 419578; H57546; Hs.49768; ESTs; mela, sarc; diag
 419687; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb
 419693; AA133749; Hs.301350; FXYD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
 419721; NM_001650; Hs.315369; aquaporin 4; glo, lung, fibro; mAb
 80 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA ; blad, headnk; diag
 419749; X73608; Hs.93029; sparcosfemecin, cwcv and ka; pros, panc, lung; diag
 419752; AA249573; Hs.152618; ESTs, Moderately similar to ZN; lung; diag

- 419B39; U24577; Hs.93304; phospholipase A2, group VII (p; pros, lung; diag
 419870; AW403911; Hs.206175; phosphoprotein associated with; mela; diag
 419875; AA853410; Hs.9357; proenkephalin; sarc; diag
 419948; AB041035; Hs.93847; NM_016931; Homo sapiens NADPH o; angio; mAb
 419956; AL137939; Hs.40086; cadherin 19, type 2; mela; mAb
 419988; X04430; Hs.93913; interleukin 6 (interferon, bet; lung, panc, esoph; diag
 419981; AA897581; Hs.128773; ESTs; angio; diag
 420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
 420062; AW411096; Hs.94785; TGF(beta)-induced transcriptor; test; CTL+s.m.
 420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
 420137; AA308478; Hs.93327; CD3D antigen, delta polypeptide; fibro; mAb
 420154; AL038155; Hs.95420; G antigen family C1 protein (pros, iso); CTL+s.m.
 420174; AL284144; Hs.199749; ESTs; angio; CTL+s.m.
 420208; BE276055; Hs.95972; silver (mouse homolog) like; mela, sarc; mAb
 420209; AA256444; Hs.126485; hypothetical protein FLJ12804; angio; diag
 420218; AW958037; Hs.381105; ribosomal protein L4; mela, pros; diag
 420255; NM_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb
 420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin; angio, fibro; mAb
 420257; N37030; Hs.173337; ESTs; mela, sarc; diag
 420281; AL0823693; Hs.323494; Predicted efflux efflux pump; lung, blad, ovar, panc; mAb
 420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; mela; diag
 420338; AAB25595; Hs.88269; Homo sapiens, clone MGC:17339; mela; mAb
 420340; NM_000724; Hs.97087; CD3Z antigen, zeta polypeptide; fibro; mAb
 420344; BE453721; Hs.97104; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
 420347; AL038539; Hs.97124; Human DNA sequence from clone ; test; diag
 420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag
 420367; AA259090; Hs.257028; ESTs; test; diag
 420376; AL137471; Hs.97265; protocadherin 18; sarc; mAb+s.m.
 420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
 420380; AA640891; Hs.102406; ESTs; lung; diag
 420424; AB033096; Hs.97594; KIAA1210 protein; pros; diag
 420462; AF050147; Hs.97932; chondromodulina I precursor; lung, EWS, sarc; mAb
 420474; LO9753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
 420544; AA877577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag
 420598; NM_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.
 420633; NM_014581; Hs.2744480; odorant-binding protein 2B (OB; breast, endo; diag
 420656; AA279098; Hs.187638; ESTs; fibro; diag
 420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
 420729; AW964897; Hs.280825; ESTs; pros; diag
 420757; X78592; Hs.99815; androgen receptor (dihydrotest; pros; mAb+s.m.
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 ft; test; diag
 420783; AL659838; Hs.99823; lectin, galactoside-binding, s; lung, blad, headnk; diag
 420789; AL870057; Hs.199882; ESTs; renal; diag
 420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
 420868; AL049874; Hs.101261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
 420923; AF097021; Hs.273321; differentially expressed in her, blad, colon; diag
 420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, mela; diag
 420981; LA0904; Hs.100724; peroxisome proliferative actv; colon; mAb+s.m.
 421016; AA504583; Hs.101047; transcription factor 3 (Ig2A fm; test; CTL+s.m.
 421044; AF081871; Hs.101302; Human DNA sequence from clone ; panc; diag
 421059; AL654133; Hs.352247; thyroid receptor interacting p; pros; mAb+s.m.
 421064; AL245432; Hs.101382; tumor necrosis factor, alphas-1; blad, uter; diag
 421070; AA283185; Hs.193327; ESTs; blad; diag
 421100; AW351838; Hs.124680; Homo sapiens cDNA: FLJ21763 ft; blad; diag
 421133; AA814977; Hs.28410; ESTs; lung; diag
 421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 ft; BPH; diag
 421155; H87879; Hs.102267; hsgl oxidase; headnk, panc, renal, sarc; diag
 421218; NM_008499; Hs.72912; cytochrome P450, subfamily 1 (blad, angio; diag
 421233; AA209534; Hs.264243; tetraspan NET-6 protein; pros, breast, ovar; mAb
 421241; X91817; Hs.102868; transketolase-like 1; test; s.m.
 421302; T34462; Hs.103201; neuritin; uter, endo ; diag
 421305; BE397354; Hs.324830; diphtheria toxin resistance pro; over; diag
 421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp5; breast, lung, angio, test, sarc; diag
 421341; AJ243212; Hs.279811; deleted in malignant brain tum; panc, lung; diag
 421350; AW301608; Hs.278188; ESTs; Moderately similar to IS; test; diag
 421373; AA808229; Hs.222088; ESTs; blad; diag
 421433; AL829192; Hs.22380; ESTs; pros; diag
 421451; AA291377; Hs.60831; ESTs; over, blad, lung; diag
 421456; NM_003654; Hs.104576; carbohydrate (keratan sulfate ; sarc; s.m.
 421478; AL663243; Hs.97258; ESTs; Moderately similar to S2; over, blad, renal, rter; diag
 421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
 421502; AF111856; Hs.105039; solute carrier family 34 (sodi); over, fibro; mAb
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
 421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, mela; CTL+s.m.
 421535; AB002359; Hs.105476; phosphoribosylformylglycaminid; test; s.m.
 421537; BE583488; Hs.105647; neural proliferation, differen; pros; diag
 421566; NM_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.
 421579; NM_002975; Hs.105327; stem cell growth factor; lymph; sarc; mAb
 421633; AF121860; Hs.106260; sorting nexin 10; mela; diag
 421650; AA781795; Hs.343800; ESTs; mela; diag
 421666; AL035260; Hs.1408; endothelin 3; mela; diag
 421727; Y13153; Hs.107318; kynurene 3-monooxygenase (ky; breast; s.m.

- 421773; W69238; Hs.112457; ESTs; mela, esoph, sarc; diag
 421777; BE552088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
 421779; AI079159; Hs.108219; wingless-type MMTV integration; colon, ovar; diag
 421796; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.
 5 421814; L12350; Hs.108623; thrombospondin 2; panc; diag
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 421887; AW161450; Hs.109201; CGI-88 protein; pros; mAb
 421898; NG2293; Hs.45107; ESTs; pros; diag
 10 421917; AB028943; Hs.109445; KIAA1020 protein; test; diag
 421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb
 421924; BE614514; Hs.109506; coronin, actin-binding protein; fibro; diag
 421946; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, mela; diag
 421952; AA300900; Hs.88849; dynein light chain 2B (DNLC2B); fibro; diag
 15 421991; NM_014918; Hs.110488; KIAA0590 protein; panc; diag
 421996; AW583807; Hs.1480; glucagon; panc; diag
 422002; X70070; Hs.110642; neurokinin receptor 1 (high s; colon; mAb
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glo; mAb
 20 422087; X58968; Hs.111301; matrix metalloproteinase 2 (pe; sarc; diag
 422089; AA523172; Hs.103135; ESTs; Weakly similar to SFR4_H; pros; diag
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
 422095; AB868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
 422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.
 25 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
 422110; AI376736; Hs.121555; secreted protein, acidic, cyst; panc; diag
 422119; AI277829; Hs.111882; KIAA0590 gene product; blad; diag
 422134; AW179019; Hs.112110; mitochondrial ribosomal protein; lung; diag
 422152; AA09249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
 30 422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 422164; NM_014312; Hs.112377; cortil al thymocyte receptor 1; blad; mAb+s.m.
 422168; AA585894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.
 422170; AI791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag
 422173; BE385828; Hs.250519; phorbolin-like protein MDS019 ; mela; diag
 35 422247; U18244; Hs.113602; solute carrier family 1 (high ; blad; mAb
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog ; ovar, headnk, blad, cerv, lung, panc, stom; mAb
 422309; U79745; Hs.114924; soluble cancer family 16 (mono; mela; mAb+s.m.
 422311; AF073515; Hs.114948; cytokine receptor-like factor ; lung, fibro; diag
 422355; AW403724; Hs.300697; coagulation factor VII (serum ; fibro; diag
 40 422363; TS5979; Hs.115474; replication factor C (activator; mela, colon; diag
 422398; AF476149; Hs.334488; hypothetical protein FLJ21992; fibro; CTL+s.m.
 422408; AF025441; Hs.116206; Ope-interacting protein 6; blad, lung; diag
 422420; U03398; Hs.1524; tumor necrosis factor (ligand; colon, panc, stom, leuk; mAb
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, ; lung, headnk; s.m.
 45 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
 422532; AI008726; Hs.118126; protective protein for beta-ga; renal, mela; s.m.
 422565; BE269035; Hs.118400; cinged (Drosophila)-like (sea ; panc, test, mela; diag
 422573; AW129798; Hs.1572; facioigenital dysplasia (Aarskog; test; diag
 422596; AF063611; Hs.118633; 2'-S'-oligoadenylate synthetase; esoph, mela; s.m.
 50 422603; BE242507; Hs.118651; hematopoietically expressed ho; angio; CTL+s.m.
 422633; X68832; Hs.198804; enolase 3, (beta, muscle); sarc; s.m.
 422658; AF231981; Hs.250175; homolog of yeast long chain pc; pros; diag
 422689; AW856665; Hs.298797; gB; RC3-CT0287-2B0100-013-d03 C; test; diag
 55 422728; U11890; Hs.1572; facioigenital dysplasia (Aarskog; test; diag
 422728; AW937626; Hs.103282; MAD (mothers against decapent; pros; diag
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
 422833; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag
 422871; AI031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
 422887; AF751846; Hs.49215; ESTs; sarc; CTL+s.m.
 60 60 422938; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
 422963; M73141; Hs.13234; ESTs; lung, panc; diag
 422997; BE018212; Hs.122908; DNA replicator factor; test; CTL+s.m.
 423017; AW179781; Hs.2227948; serine (or cysteine) proteinases; blad, headnk, mela; mAb+diag
 423052; M26214; Hs.123072; RAB5B, member RAS oncogene fam; pros; diag
 65 423189; M59371; Hs.171556; EphA2; colon, ovar; mAb
 423195; AK001866; Hs.128139; hypothetical protein FLJ1104; fibro; CTL+s.m.
 423196; M61933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
 423201; NM_000163; Hs.126180; growth hormone receptor; pros; mAb
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung, esoph; diag
 423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent; test, fibro; mAb
 423387; AJ012074; Hs.348500; vasoactive Intestinal peptide ; pros; mAb
 423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb
 70 423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glo; mAb+CTL
 423445; NM_014324; Hs.128748; alpha-methylacyl-CoA racemase; pros; s.m.
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
 75 423458; AI204212; Hs.351113; ESTs; test; CTL+s.m.
 423511; AF036329; Hs.129715; gonadotropin-releasing hormone; lung; diag
 423515; AA327017; Hs.176594; ESTs; ovar; diag
 423541; AA296922; Hs.129770; serine protease inhibitor, Kaz; colon, panc; diag
 80 423575; C18863; Hs.163443; Intron of peroxins (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047828; Hs.129887; cadherin 19, type 2; mela; mAb
 423842; AW452850; Hs.157148; hypothetical protein MGC13204; lung; diag
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc finger); lung; diag
 423685; BE350494; Hs.49753; uveal autoantigen with collet ; panc, uter, colon; CTL+s.m.
 5 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
 423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag
 423761; NM_006194; Hs.132576; paired box gene 9; headnk; CTL+s.m.
 10 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
 423778; Y09287; Hs.132821; Bavin containing monooxygenases; fibro; s.m.
 423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glo; diag
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test, esoph; diag
 423788; AF047033; Hs.132904; solute carrier family 4, sodium; angio; mAb
 423799; AW028300; Hs.132906; 19A24 protein; mela; mAb
 15 423849; AL167426; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
 423887; AL080207; Hs.134585; DKFZP434C232 protein; headnk, lung; diag
 423899; NM_001427; Hs.134989; engrailed homolog 2; mela; CTL+s.m.
 423905; AW579960; Hs.135150; lung type-I cell membrane-assoc; test; mAb
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, me; test; diag
 20 423934; U88995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag
 424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
 424036; AA770568; Hs.348495; H2A histone family, member L; pano, ovar; CTL+s.m.
 25 424054; AA334511; Hs.266338; membrane-spanning 4-domains, s; pros, fibro; mAb
 424078; AB008625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); test; diag
 424096; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
 424125; M31669; Hs.1735; inhibin, beta B (activin AB be; ovar, pros; diag
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
 424153; AA451737; Hs.141496; MAGE-like 2; mela; CTL+s.m.
 30 424165; AW582904; Hs.142256; islet amyloid polypeptide; panc; mAb
 424212; NM_005814; Hs.143131; glycoprotein A33 (transmembrane; colon, stom, ovar; mAb
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); mela, fibro; diag
 424244; AV647184; Hs.143601; hypothetical protein hCLIA-iso; blad; diag
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
 35 424264; D80400; Hs.239388; Human DNA sequence from clone ; blad; mAb
 424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
 424310; AA388648; Hs.50334; testes development-related NYD; fibro; diag
 424332; AA388919; Hs.101615; ESTs; pros; diag
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
 40 424343; AW595360; Hs.4748; adenylate cyclase activating p; glo, ovar, uter; mAb
 424384; AW383226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag
 424420; BE614743; Hs.146888; prostaglandin E synthase; lung, blad; s.m.
 45 424440; AA340743; Hs.133208; ESTs; sarc; diag
 424441; X14860; Hs.147097; H2A histone family, member X; lung; diag
 424450; AL137520; Hs.149472; dynein intermediate chain 2; fibro; diag
 424522; AL134847; Hs.149957; nitoosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
 50 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag
 424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.
 424581; M52062; Hs.150917; casinin (cadherin-associated pr; glo, ovar, uter; mAb+s.m.
 424588; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
 424629; M80858; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
 424635; AA420607; Hs.115455; Homo sapiens cDNA FLJ14250 f1c; glo; diag
 55 424676; Y08565; Hs.151676; UDP-N-acetyl-alpha-D-galactos; breast; s.m.
 424704; AI263293; Hs.152098; cytochrome P450, subfamily II; renat; s.m.
 424711; NM_005795; Hs.152175; calcitonin receptor-like; angio; mAb
 424717; H03754; Hs.152213; wingless-type MMTV integration; blad, lung, headnk; diag
 424800; AL035589; Hs.153203; MyoD family Inhibitor; test, pros; diag
 60 424806; AA382523; Hs.153408; MSTPO31 protein; angio; mAb
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 f1c; lung, blad, ovar, headnk, esoph, cerv, uter; diag
 424846; AU077324; Hs.1832; neuropeptid Y; pros; diag
 424897; D63216; Hs.153684; frizzled-related protein; panc; EWS, stom, renat; diag
 424902; NM_003866; Hs.153687; inositol polyphosphate-4-phosph; panc, leuk, mela; CTL+s.m.
 65 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni; mela, colon; CTL+s.m.
 424971; AA479005; Hs.154036; tumor suppressing subunit; panc, mela; CTL+s.m.
 424998; US8515; chitinase 3-like 2; glo; diag
 425023; AW956689; Hs.154210; EDG-1 (endothelial different); angio; mAb
 425048; H05468; Hs.164502; ESTs; lung, blad; diag
 70 426057; AA28434; Hs.1619; arachael-scuta complex (Drosoph; glo, lung; CTL+s.m.
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glo, mela; diag
 425164; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
 425200; BE255203; comp; Hs.165101; ATP synthase, H transporing; ; panc; s.m.
 75 425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
 425211; M16667; Hs.1867; progastrinsin (pepsinogen C); fibro, esoph, pros; diag
 425234; AW152226; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, mela; diag
 425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 f1; angio; diag
 425237; U07695; Hs.155227; EphB4; test; mAb
 80 425245; AI751768; Hs.155314; KIAA0095 gene product; lung; diag
 425259; AI049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 425262; DB7119; Hs.155418; GS3955 protein; mela, renat; CTL+s.m.
 425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

425289; AW139342; Hs.155530; interferon, gamma-inducible pr; mela; CTL+s.m.
 425308; M97639; Hs.155585; receptor tyrosine kinase-like ; pros, sarc; mAb
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, ; fibro; diag
 425371; D49441; Hs.155981; mesothelin; over, lung, fibro; mAb
 5 425397; JD4088; Hs.156346; topoisomerase (DNA) II alpha ; lung, blad, panc, angio, test, mela, esoph; CTL+s.m.
 425427; A162682; Hs.317432; branched chain aminotransferase; test; s.m.
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
 425465; L18964; Hs.1904; protein kinase C, iota; over, pros, colon; s.m.
 10 425525; AA358583; Hs.23871; ESTs; sarc; diag
 425545; N98529; Hs.158295; Homo sapiens, clone MGC12401; sarc; diag
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23563 f; fibro; CTL+s.m.
 425572; AB011076; Hs.158307; undifferentiated embryonic cel; test; CTL+s.m.
 425601; AW629485; Hs.140720; GSK-3 blinding protein FRAT2; test; CTL+s.m.
 425606; US2121; Hs.158331; ranin-binding protein; mela; diag
 15 425628; NM_004476; Hs.1915; folate hydrokase (prostate-spe); pros; s.m.
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
 425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.
 425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 20 425698; NM_005401; Hs.159238; protein tyrosine phosphatase, ; lung; mAb+s.m.
 425705; AA383076; Hs.159274; outer dense fibre of sperm tail; test; diag
 425710; AF030880; Hs.159275; solute carrier family, member ; pros; mAb
 425722; A1669076; Hs.97031; hypothetical protein MGC13047; mela; diag
 425726; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
 25 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA; test; diag
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohor; test; diag
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
 425921; NM_097231; Hs.162221; solute carrier family 8 (neuro; stom, panc; mAb
 425976; C75094; Hs.334514; NG22 protein; pros, over; mAb
 30 426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
 426050; AF017307; Hs.166096; ET4-like factor 3 (ets domain; over, blad, stom; CTE+s.m.
 426059; BE202842; Hs.166120; Interferon regulatory factor 7; esoph, cerv; CTL+s.m.
 426057; AW654691; Hs.97053; ESTs; lung; diag
 426088; AF038007; Hs.166198; ATPase, Class I, type 8B, memb; blad, lung; mAb
 35 426084; AF034611; Hs.166208; cubilin (intrinsic factor-coba; renal; diag
 426116; AA668729; Hs.144694; ESTs; fibro; diag
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila; colon, stom, panc, pros, renal, fibro, cerv; mAb
 426158; BE244537; Hs.167382; natriuretic peptide receptor A; over; mAb
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic; breast, over, blad, panc, colon, fibro, mela; diag
 426172; AA371307; Hs.125056; ESTs; pros; diag
 40 426174; AA547939; Hs.115838; Homo sapiens similar to Echino; breast, pros, fibro; diag
 426212; S71824; Hs.167988; neural cell adhesion molecule ; glo; mAb
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glo; diag
 426274; D98122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb
 426300; U15979; Hs.169228; delta-like homolog (Drosophila; over, sarc; mAb
 45 426310; NM_000909; Hs.169268; neuropeptide Y receptor Y1; breast; mAb
 426312; AF026939; Hs.181874; interferon-induced protein wit; esoph, mela; diag
 426320; W47595; Hs.189300; transforming growth factor, beta; over, pros, blad, panc; diag
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
 426363; MS8524; Hs.2025; transforming growth factor, beta; pros; diag
 426370; RS9288; Hs.281706; sortilin 1; sarc; diag
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
 426440; BE382756; Hs.159902; solute carrier family 2 (faci; lung, panc, over, blad, headnk, esoph; mAb
 426462; US9111; Hs.169953; dermatan sulphate proteoglycan; sarc; diag
 50 426470; AA520734; Hs.128644; ESTs; mela; diag
 426471; M22440; Hs.170009; transforming growth factor, alpha; headnk, renal, panc; diag
 426490; NM_001621; Hs.170087; earyl hydrocarbon receptor; panc; mAb+s.m.
 426501; AW043782; Hs.239616; ESTs; pros, breast, glo, lung, mela; mAb
 426802; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag
 60 426534; US6096; Hs.2051; testis specific protein, Y-in; test; CTL+s.m.
 426535; AU077012; Hs.170279; ESTs; Weekly similar to ubiqui; angio; diag
 426555; NM_000372; Hs.2053; tyrosinase (oculocutaneous albi; mela, sarc; mAb
 426559; AB001914; Hs.170414; paired basic amino acid cleav; hepC, breast, over, renal; diag
 426575; MT4826; Hs.170508; glutamate decarboxylase 2 (panc, panc; s.m.
 65 426627; AF012359; Hs.195685; ESTs; test; diag
 426635; BI395109; Hs.129327; hypothetical protein MGC13057; over; CTL+s.m.
 426682; AW660038; Hs.2056; UDP glycosyltransferase 1 fam; blad, lung; s.m.
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase ; over; CTL+s.m.
 426696; AW383332; Hs.171844; Homo sapiens cDNA: FLJ22298 f; angio; mAb
 70 426721; AA383588; Hs.288545; ESTs; Weekly similar to T29012; fibro; diag
 426728; AA488915; Hs.171955; trophom associated protein ; test; diag
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
 426752; X69490; Hs.172004; titin; sarc; diag
 426759; AI590401; Hs.21213; ESTs; mela; diag
 75 426793; X889817; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.
 426822; NM_000020; Hs.1722670; activin A receptor type II-lik; angio; mAb
 426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
 426897; AW976570; Hs.97387; ESTs; lung; diag
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
 80 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.
 426966; AI49314; Hs.349204; sclerostin; lung; diag
 426968; UD7618; Hs.173034; amphiphysin (Sif-Mann syndro; blad; mAb+CTL
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 f; over, sarc; diag
 427050; AW68287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

- 427099; AB032853; Hs.173560; odd Oz/len-m homolog 2 (Drosop; headnk, esoph; diag
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb
 427244; AA402400; Hs.178045; ESTs; esoph; diag
 427260; AA663848; gbae70b06.s1 Stratagene schiz; lung; diag
 5 427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros; carc; mAb
 427290; AA400485; ESTs; test; diag
 427316; AF186081; Hs.175783; zinc transporter; pros; mAb
 427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
 10 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin); ovar; mAb
 427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
 427398; AW390020; Hs.20416; chromosome 21 open reading fr; pros; diag
 427427; AF077345; Hs.177936; lecili superfamily member 1 ; breast; diag
 15 427441; AA412805; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
 427461; AA531527; Hs.332040; hypothetical protein MGC1301C; pros; mAb
 427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfate; carc; diag
 427486; AA974433; Hs.362432; fibroblast growth factor 4 (ne; test; diag
 427510; ZA7542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
 20 427515; T79526; Hs.179516; integral type I protein; pros; diag
 427521; AW973352; ESTs; test; diag
 427528; AI077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.
 427535; R28543; Hs.2164; pro-platelet basic protein (lin; fibro; diag
 427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
 427550; BE242918; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.
 25 427557; NM_002659; Hs.179657; plasmaminogen activator, unknoing pane, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
 427583; MB2952; Hs.179704; meprin A, alpha (PABA peptide ; colon; mAb
 427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, carc; diag
 30 427615; BE410107; Hs.179817; CGI-82 protein, PSDR1; pros; diag
 427634; AI359745; Hs.18449; hypothetical protein MGC10820; mela, carc; diag
 427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fs; carc; diag
 427668; AI791495; Hs.180142; calmodulin-like skin protein ; breast, cerv, blad, lung, headnk, esoph; diag
 427667; AK001278; Hs.180171; Homo sapiens cDNA FLJ10417 fs; test; diag
 35 427680; AA298760; Hs.180181; hypothetical protein FLJ14904; lung, test; diag
 427681; AB018265; Hs.284232; tumor necrosis factor receptor; ovar; mAb+CTL
 427692; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.
 427701; AA411101; Hs.243888; nuclear autoantigenic sperm pr; lung; mAb+CTL
 427716; BE245274; Hs.180428; KIAA1181 protein; pros; diag
 40 427719; AI33122; Hs.134726; ESTs; test, blad; diag
 427730; AW250549; Hs.180577; granulin; mela; diag
 427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
 427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
 427811; M31057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.
 45 427897; NM_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag
 427912; AI022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
 427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
 427961; AW293165; Hs.143134; ESTs; lung, carc; diag
 428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag
 428004; AA449583; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
 50 428023; AI038B43; Hs.374630; Homo sapiens cDNA: FLJ23602 fs; lung; diag
 428046; AW812795; Hs.337534; ESTs, Moderately similar to 18; lung, colon ; diag
 428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
 428087; AA100873; Hs.182421; troponin C2, fast; carc; CTL+s.m.
 428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb
 55 428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 428169; AI928984; Hs.182793; golgi phosphoprotein 2; pros; diag
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, carc; CTL+s.m.
 428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 60 428208; AB020843; Hs.183008; KIAA0836 protein; angio; mAb
 428221; U95781; Hs.193076; ATPase, Ca transporting, card; carc; s.m.
 428227; AA321649; Hs.2248; small inducible cytokine subf; breast, lung, blad, over, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag
 428248; AI126772; Hs.40479; ESTs; carc; diag
 428293; BE250844; Hs.183556; solute carrier family 1 (neut; pros; mAb
 65 428305; AA446626; Hs.2739; cartilage linking protein 1 ; carc; diag
 428320; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
 428333; AA503115; Hs.183752; microseminoprotein, beta; pros; diag
 428365; BE266452; Hs.2257; vitronectin (serum spreading C; colon; diag
 428398; AI249358; Hs.985558; ESTs; pros, breast ; diag
 70 428405; Y00762; Hs.2266; cholinergic receptor, nicotinic; esoph, carc; mAb
 428422; AU078517; Hs.184276; solute carrier family 9 (sod1); ovar; CTL+s.m.
 428434; AW363590; Hs.85551; Homo sapiens, Similar to DNA s; lung, fibro; diag
 428457; AK002121; Hs.184465; hypothetical protein FLJ11269; fibro; mAb
 428471; X57348; Hs.184510; atratin; lung, headnk, colon, panc; diag
 428545; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.
 75 428651; AF195478; Hs.188401; annexin A10; blad, stom, panc; diag
 428667; AI375550; Hs.346868; nuclear protein p40; homolog; fibro, uter, diag
 428722; U76456; Hs.190787; tissue inhibitor of metalloprotein; glio; diag
 428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
 80 428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
 428784; Y12851; Hs.183470; purinergic receptor P2X, ligand; glio, mela; mAb
 428800; M57627; Hs.193717; interleukin 10; fibro; diag
 428801; AW277121; Hs.254881; ESTs; pros; diag
 428804; AK000713; Hs.193736; hypothetical protein FLJ20706; mela; diag

428810; AF068236; Hs.193708; nitric oxide synthase 2A (indu; lung; s.m.
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
 428824; W23624; Hs.173059; ESTs; panc; diag
 428832; AA570229; Hs.324239; ESTs; Moderately similar to ZN; panc; uter; diag
 5 428841; AI118430; Hs.104935; ESTs; renal; diag
 428848; NM_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag
 428862; NM_000346; Hs.2316; SRY (sex determining region Y); pros; sarc; CTL+s.m.
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
 10 428928; BE49838; Hs.194657; cadherin 1, type 1, E-cadherin; pros; breast; stom; blad; mAb
 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
 428957; NM_003881; Hs.194679; WNT1 inducible signaling pathway; cerv; diag
 428959; AF100779; Hs.194680; WNT1 inducible signaling pathway; sarc; diag
 428977; AK001404; Hs.194688; cyclin B2; test; CTL+s.m.
 15 428981; BE313077; Hs.93135; ESTs; Weakly similar to ALU2_H; sarc; diag
 429002; AW248439; Hs.2340; Junction plakoglobin; blad; CTL+s.m.
 429010; Y18198; Hs.194725; one cut domain, family member ; panc; diag
 429013; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
 429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag
 20 429066; AI753247; Hs.29843; Homo sapiens cDNA FLJ13103 fc; lung; diag
 429083; Y09397; Hs.227817; BCL2-related protein A1; mela; diag
 429113; D28235; Hs.196384; prostaglandin-endoperoxide synth; anglo; blad, stom; s.m.
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolo; ovar; mAb
 25 429163; AA884765; gb:am20a10.1|Soares_NFL_L_GBC; pros; diag
 429170; NM_001394; Hs.2358; dual specificity phosphatase 4; breast; panc; stom; lung; mela; s.m.
 429201; X03178; Hs.198246; group-specific component (vitz); panc; diag
 429220; AW207208; Hs.356962; ESTs; breast; pros; BPH; diag
 429228; AI553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
 30 429259; AA420450; Hs.380088; Plakophilin; lung, headnk; diag
 429290; AF203032; Hs.198760; neurofiliament, heavy polypept; pros; CTL+s.m.
 429299; AI620463; Hs.347408; hypothetical protein MGC13102; pros; cerv; diag
 429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3); sarc; mAb
 429345; R11141; Hs.199695; hypothetical protein; blad; diag
 35 429359; W00482; Hs.2399; malix metalloproteinase 14 (m; headnk; breast, cerv, ovar, blad, lung, esoph, mela, sarc; mAb
 429413; NM_014058; Hs.201877; DESC1 protein; lung; blad; diag
 429415; NM_002593; Hs.202097; procollagen C-endopeptidase enz; sarc; diag
 429423; AI016712; Hs.380983; integrin, beta 1 (fibronectin ; anglo; mAb
 429432; AI678059; Hs.202676; synaptosomal complex protein 2; breast; cerv; diag
 40 429441; AJ224172; Hs.204096; fibrophilin B (tercoglobin fam); breast; pros; ovar; diag
 429466; MB5838; Hs.12827; ESTs; glo; uter; CTL+s.m.
 429469; MG64500; Hs.380791; glycine dehydrogenase (decarbo); test; s.m.
 429486; AF155827; Hs.203953; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
 429500; X78565; Hs.289114; hexabrachion (tenascin C); cyto; lung, glo, headnk, mela, sarc; diag
 429504; X89133; Hs.204238; Spocella 2 (oncogene 24p3) (N; ovar, lung, blad; diag
 429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
 429563; BE619413; Hs.2437; eukaryotic translation Initia; lung; diag
 429566; T73510; Hs.208153; angiopoietin-like 3; hepC; CTL+s.m.
 50 429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc; colon, stom, lung; mAb
 429609; AF002246; Hs.210863; cell adhesion molecule with ho; ovar, mela; diag
 429612; AF062649; Hs.252887; pituitary tumor-transforming 1; lung, blad, headnk; diag
 429655; U468959; Hs.211582; myosin, light polypeptide kinase; pros; s.m.
 55 429663; MB5874; Hs.211587; phospholipase A2, group IV A (c; anglo, lung; s.m.
 429664; L20433; Hs.211588; POU domain, class 4, transcrp; sarc; CTL+s.m.
 429736; AF126304; Hs.212680; tumor necrosis factor receptor; lung; mAb
 429747; M07507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
 429769; NM_004917; Hs.218366; kallikrein 4 (prostase, enamel; pros; s.m.
 60 429784; M89796; Hs.30; membrane-spanning 4-domains; s; fibro; mAb
 429823; AA459443; Hs.181400; ESTs; sarc; diag
 429859; NM_007050; Hs.225952; protein tyrosine phosphatase; ; breast; mAb+s.m.
 429916; AW873986; Hs.119383; ESTs; pros; glo; diag
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
 65 429983; W92820; Hs.260855; ESTs; blad; diag
 429986; AF092047; Hs.227277; sine oculis homeobox (Drosoph); lung; CTL+s.m.
 430014; H59354; Hs.374303; actinin, alpha 4; rensl; diag
 430016; NM_004738; Hs.227656; xenotropic and polytropic retr; ovar; mAb
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
 70 430056; X97548; Hs.228695; KRAB-associated protein 1; test; CTL+s.m.
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; anglo; diag
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
 430144; AI732722; Hs.58927; ERGIC-53-like pr; pros; diag
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
 430164; AW583058; Hs.234728; serine (or cysteine) proteinases; pros; diag
 75 430157; BE348706; Hs.278543; ESTs; blad; diag
 430168; AW583343; Hs.145582; DKFZP434I1735 protein; blad; diag
 430223; NM_002514; Hs.235835; nephroblastoma overexpressed 9; mela; diag
 430226; BE245562; Hs.2551; adrenergic, beta-2, receptor; pros; mAb
 430228; AW950939; Hs.6392; ESTs; Highly similar to T00391; glo; diag
 430252; AI638774; Hs.106326; testes development-related NYD; test; CTL+s.m.
 80 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
 430259; BE550182; Hs.375142; RafGEF-like protein 3, mouse h; ovar; CTL+s.m.

- 430280; AA361258; Hs.237888; Interleukin 7 receptor; mela, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
 430287; AW182459; Hs.125769; ESTs, Weakly similar to LEU5_H; test; diag
 430294; AI53B226; Hs.32976; guanine nucleotide binding pro; pros; diag
 430337; M36707; Hs.239600; calmodulin-like 3; lung; diag
 5 430354; AA854810; Hs.239784; human homolog of Drosophila Ssc; ovar; diag
 430378; Z29572; Hs.2558; tumor necrosis factor receptor; lung,fibro, breast headnk, blad, breast, colon, stom; diag
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
 430396; D49742; Hs.241353; hyaluronan-binding protein 2; panc; diag
 430407; H23551; Hs.30974; ESTs; panc; diag
 10 430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
 430454; AW469011; Hs.105635; ESTs; lung; diag
 430476; AAA47465; Hs.2563; tachykinin, precursor 1 {subst; sarc; diag
 430487; D87742; Hs.241652; KIAA0268 protein; pros; diag
 15 430491; AL109791; Hs.241539; Homo sapiens mRNA full length ; ovar; diag
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup); leuk; diag
 430508; AI015436; Hs.104637; ESTs; lung; mAb+s.m.
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
 20 430540; AW245422; Hs.106357; Homo sapiens cDNA FLJ22105 f; mela; mAb
 430583; AAA81289; Hs.348626; ATP-binding cassette, sub-fam1; lung; diag
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mela; diag
 430634; AIB60651; Hs.26865; calcyphosine; ovar; diag
 430837; BE160081; Hs.256290; S100 calcium-binding protein A; mela; diag
 430647; AC003682; Hs.127988; ESTs, Weekly similar to Z211_H; test; diag
 25 430676; AF084966; Hs.372585; gbt:Homo sapiens envelope prote; test; diag
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
 430578; AI458174; Hs.192855; ESTs; lung; diag
 430588; NM_001942; Hs.2633; desmoglein 1; lung, headnk, mela; mAb
 30 430691; C14187; Hs.157209; aristaless-related homeobox pr; EWS, ovar, panc; diag
 430704; AW813091; Hs.335799; ESTs; stom; diag
 430770; AA765694; Hs.123296; ESTs; mela; diag
 430832; AI073913; Hs.100586; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
 430838; N46654; Hs.163395; hypothetical protein FLJ12015; mela; CTL+s.m.
 35 430850; X54232; Hs.2689; glyptican 1; glio, lung, cerv, blad, esoph; mAb
 430985; AA490232; Hs.27323; ESTs, Weakly similar to I78986; lung; mAb
 431009; BE149762; Hs.48956; gap junction protein, beta 6 {; lung, blad, headnk, esoph; mAb
 431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
 40 431089; BE041395; Hs.374629; ESTs, Weakly similar to unkown; blad, lung, pros, anglo, fibro; diag
 431093; Y13367; Hs.249235; phosphoinositide-3-kinase, clif; pros; CTL+s.m.
 431103; M57399; Hs.44; pleiotrophin (heparin binding ; sarc, mela; diag
 431124; AF284221; Hs.59506; doublesex and mab-3 related t5; lung; CTL+s.m.
 431125; BE197083; Hs.366053; gba1a1d10.y1 NIH_MGC_7 Homo s; pros; mAb
 431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.
 45 431183; NM_006855; Hs.2501696; KDE (Lys-Asp-Glu-Leu) endopeptidase; mela, pros, panc, colon, stom; mAb
 431211; M86849; Hs.323733; gap junction protein, beta 2 ; colon, blad, lung, panc, headnk, esoph; mAb
 431217; NM_013427; Hs.250830; Rho GTPase activating protein ; pros; CTL+s.m.
 431221; AA449016; Hs.286145; SRB7 (strespresso of RNA polymer; lung; CTL+s.m.
 431222; X56777; Hs.273780; zona pellucida glycoprotein 3A; pros; diag
 50 431250; BE264648; Hs.251577; taxol resistance associated ga; esoph; diag
 431322; AW970622; Hs.376626; cb; EST382704 MAGE resequences; blad, ovar, uter; diag
 431347; AI133461; Hs.251684; insulin-like growth factor 2 {; blad; mAb+diag
 431354; BE046956; Hs.251673; DNA (cytosine-5-)methyltransfer; test; CTL+s.m.
 431360; NM_000427; Hs.251680; kitorin; mela, sarc; diag
 55 431362; AI874223; Hs.283560; ESTs; anglo; diag
 431369; BE184455; Hs.251754; secretory leukocyte protease l; ovar, blad; diag
 431384; BE158000; Hs.334372; gbt:MRP-2HT0377-150200-202-e03 H; lung; diag
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
 431441; UB1961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
 60 431446; AL137517; Hs.308204; hypothetical protein DKFZp564O; blad; mAb
 431457; NM_012211; Hs.256297; integrin, alpha 11; headnk; mAb
 431474; AL133990; Hs.190542; CEGP1 protein; breast, pros, blad; diag
 431494; AA891355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
 65 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
 431548; AI034273; Hs.9711; novel protein; lung, anglo, pros; diag
 431553; X78075; Hs.2789; cartilage linking protein 1; sarc; diag
 431579; AW971082; Hs.222886; ESTs, Weekly similar to TRHY_H; pros; diag
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon ; mAb
 431674; AA088901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
 70 431723; AW0583350; Hs.278986; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
 431728; NM_007351; Hs.268107; multinem; anglo; diag
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
 431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme ; mela; mAb
 431870; AW449902; Hs.105500; ESTs; renal; diag
 75 431890; X17033; Hs.271985; integrin, alpha 2 (CD49B, alphi; blad, headnk, lung, panc, cerv, stom; mAb
 431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag
 431939; AW008081; Hs.231994; ESTs; renal, colon; diag
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 f; cerv, glio; diag
 431989; AW972870; Hs.291069; ESTs; ovar; diag
 80 431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.
 432004; BE018302; Hs.2894; placental growth factor, vaso; renal; diag
 432015; AL157604; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 432117; AL036195; Hs.2909; proline 1; test; CTL+s.m.
 432126; AA127221; Hs.66; ESTs; angio; diag
 432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.
 5 432189; AA527941; ; gb:nh30c04.s1 NCI_CGAP_P3 Hom; pros; diag
 432189; AI698815; Hs.127179; cryptic gene; panc; diag
 432210; AI567421; Hs.27330; Homo sapiens, clone IMAGE-3544; ovar, lung, blad; diag
 432222; AJ204995; ; gb:an03c03x1 Stralagene schiz; angio, blad, fibro; diag
 432231; AA359977; Hs.274127; CLST 11240 protein; fibro; diag
 10 432239; X81334; Hs.2906; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.
 432240; AI694767; Hs.129178; Homo sapiens cDNA FLJ13581 fts; pros; diag
 432305; M62402; Hs.274313; insulin-like growth factor bln; cerv; diag
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fts; cerv, lung, fibro, pros; diag
 15 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2; lung, test, colon; diag
 432415; T16971; ; ESTs; Weakly similar to A43932; ovar, pros; diag
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag
 432455; BE218866; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear f; blad, fibro, pros; diag
 20 432473; AI202703; Hs.152414; ESTs; pros; diag
 432481; AW451645; Hs.151504; intron of collagen, type XI, a; sarc; diag
 432512; NM_003284; Hs.3017; translation protein 1 (during h; test; CTL+s.m.
 432519; AI2221311; Hs.130704; ESTs, Weakly similar to BCHUA; fibro, ovar, uter; CTL+s.m.
 432527; AW875028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag
 25 432542; AW0083920; Hs.16098; claudin 2; colon, panc; diag
 432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
 432616; AA557191; Hs.65028; ESTs, Weakly similar to IS4374; pros; diag
 432621; AI298501; Hs.21192; ESTs, Weakly similar to T46428; pros; mAb
 432629; AW860548; Hs.280658; ESTs; ovar; diag
 30 432653; N62096; Hs.293185; ESTs, Weakly similar to JC732B; pros, lung ; mAb+s.m.
 432666; AW204069; Hs.351118; ESTs, Weakly similar to unname; test; diag
 432706; NM_013230; Hs.286124; CD24 antigen (small cell lung ; colon, ovar, pros; mAb+CTL
 432730; AI066520; Hs.131358; ESTs; test; diag
 432731; F31178; Hs.287820; fibronectin 1; panc, fibro; diag
 35 432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ29117 f; lung, ovar; CTL+s.m.
 432800; BE391046; Hs.278962; AIM-1 protein; mela; pros; mAb
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); telo; mAb
 432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
 432857; AW016836; Hs.233364; ESTs; stom, colon; diag
 40 432878; BE386490; Hs.279663; Print; mela; CTL+s.m.
 432887; AI026047; Hs.162859; Homo sapiens cDNA FL; pros; diag
 432938; T27013; Hs.3132; steroidogenic acute regulatory; over; diag
 432988; AA650114; Hs.326198; ESTs; pros; diag
 45 433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, y; mela; diag
 433013; AI697890; Hs.127337; axin 2 (conductin, axil); colon; CTL+s.m.
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 433088; NM_006456; Hs.288215; sialytransferase; breast, ovar, mela; s.m.
 433078; AW015188; Hs.121579; Homo sapiens cDNA FLJ12231 fts; blad; diag
 50 433091; Y12842; Hs.3105; lymphocyte antigen 6 complex ; blad, lung, headnk, cerv; mAb
 433147; AF091434; Hs.43080; platelet derived growth factor; over, panc, fibro; diag
 433159; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag
 433170; AB037816; Hs.8982; KIAA1395; angio; diag
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
 55 433228; F28212; Hs.14983; K0AA1491 protein; test; CTL+s.m.
 433250; AI806626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
 433285; AW875944; Hs.237398; ESTs; breast, pros; diag
 433299; AF007835; Hs.324117; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
 60 433323; AA805132; Hs.159142; ESTs; pros; diag
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.
 433335; AF017986; Hs.31386; secreted frizzled-related prot; over, fibro, headnk, lung, panc, blad; diag
 433364; AI075407; Hs.296083; ESTs, Moderately similar to 15; mela; diag
 433365; AF026944; Hs.293797; ESTs; blad; diag
 65 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
 433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
 433404; T32982; Hs.352670; Homo sapiens cDNA:FLJ32064 fts; pros; diag
 433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glo, colon; s.m.
 433444; AW975324; Hs.128816; ESTs; pros; diag
 70 433458; AA508353; Hs.105814; relaxin 1 (H1); pros; diag
 433485; AI493076; Hs.306098; aldo-keto reductase family 1 , lung; s.m.
 433495; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag
 433576; BE080715; Hs.161091; ESTs; mela; diag
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene; color; diag
 433571; AW138797; Hs.132306; 19A24 protein; fibro; mAb
 75 433701; AW445023; Hs.15155; ESTs; test; diag
 433724; AI827749; Hs.144924; serine/threonine protein kinases; test; CTL+s.m.
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_ ; pros, over; diag
 433800; AI034361; Hs.135150; lung type-I cell membrane-assc; glo, lung, test; mAb
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
 80 434011; AW953437; Hs.6486; clone FLB5214; pros; diag
 434105; AW952124; Hs.13094; presenilin associated rhombot; lung; diag
 434217; AW014795; Hs.23349; ESTs; angio; diag
 434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 f1; test; diag
 434340; A1193043; Hs.353146; ESTs; Weekly similar to T17226; lung; diag
 434360; AW015415; Hs.127780; ESTs; lung; diag
 434370; AF130886; Hs.56346; ectodysplasin 1, anhidrotic re; colon, stom; diag
 434377; AW137148; Hs.306593; iron overexpression (OSF-2as); headnk; diag
 434398; AA121098; Hs.3838; senan-inducible kinase (SNK); angio, breast; CTL+s.m.
 434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
 434414; AF798376; gbt834b07,x1 NCI_OGAP_Ov23 Hs; lung, test, colon; diag
 434423; NM_005769; Hs.3844; LIM domain only 4; panc; diag
 434449; AW953484; Hs.3849; hypothetical protein FLJ22041; sarc; diag
 434487; AF143867; Hs.337598; ESTs; Moderately similar to S6; blad; mAb+s.m.
 434596; 159538; gby65g12s1 Stralagene ovary; angio; s.m.
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.
 434609; R76593; gbyf60c11.r1 Soares placenta ; pros; diag
 434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40360; test; diag
 434665; AA642125; Hs.74502; gbnr60c01.s1 NCI_OGAP_Lym3 Hs; panc; diag
 434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 f5; panc; diag
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phospho; mefa; s.m.
 434846; AW295389; Hs.119768; ESTs; angio; diag
 434876; AF160477; Hs.51460; Ig superfamily receptor LNIR; lung, blad; mAb
 434927; H46512; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
 434973; AW449285; Hs.313636; EST; pros; diag
 435045; BE257155; Hs.143698; ESTs; test; diag
 435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
 435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
 435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
 435094; AI560129; Hs.289008; EST; ovar, cerv; diag
 435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, mefa; CTL+s.m.
 435140; AA668123; Hs.134170; ESTs; fibro; diag
 435159; AA668879; Hs.116649; ESTs; lung; diag
 436206; AI432364; Hs.160594; ESTs; test; diag
 435243; AW292986; Hs.348932; hypothetical protein dj434014.; cerv, headnk; diag
 435292; N20514; Hs.172965; ESTs; mefa; diag
 435299; AF745458; Hs.343026; ESTs; Weekly similar to T20593; fibro; diag
 435479; AF197137; Hs.156101; ATP synthase, H transporting; pros; s.m.
 435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
 435583; AF210317; Hs.95497; solute carrier family 2 (facil); blad; mAb+s.m.
 435575; AF213457; Hs.44234; triggering receptor expressed ; fibro; mAb+s.m.
 435602; AF217515; Hs.283532; uncharacterized bone marrow pr; test; diag
 435615; Y15065; Hs.4976; potassium voltage-gated channel; glo; mAb
 435652; N32388; Hs.334370; uncharacterized hypothalamus pr; panc; diag
 435793; AB037734; Hs.4933; KIAA1313 protein; ovar, lung, uter; diag
 435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
 435876; AW612506; Hs.160271; G protein-coupled receptor 48; pros; mAb
 435897; AF269223; Hs.128322; t-complex 1 (a murine top horn; test; diag
 435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
 435918; AF263538; Hs.86232; growth differentiation factor ; test; diag
 435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 436032; AA150707; Hs.109276; latexin protein; panc, angio; diag
 436063; AR000028; Hs.356100; ribosomal protein S24; pros; diag
 436120; AI248193; Hs.119880; ESTs; fibro; diag
 436199; K38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
 436248; AW450963; Hs.118991; ESTs; blad; diag
 436251; BE515085; Hs.296585; nucleolar protein [KKE/D repeat; colon, test, blad; CTL+s.m.
 436278; BE396290; Hs.5097; synaptojanin 2; pros; mAb
 436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
 436293; AI601166; Hs.306201; ESTs; blad; diag
 436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag
 436315; BE390513; Hs.27835; hypothetical protein MGC4837; mefa; diag
 436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag
 436420; AA443966; Hs.315995; ESTs; angio; mAb
 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
 436511; AA721252; Hs.291502; ESTs; lung; diag
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag
 436569; BE439539; Hs.301981; glutathione S-transferase M2 (-; blad; s.m.
 436614; AW104388; Hs.149091; ESTs; mefa; CTL+s.m.
 436700; AW63590; Hs.3014406; hypothetical protein PP3501; mefa; mAb
 436728; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb
 436772; AW975688; Hs.348918; metallothionein 1E (functional); angio; diag
 436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
 436838; AA767346; Hs.372277; ESTs; lung; diag
 436856; AI469355; Hs.127310; ESTs; mefa; diag
 436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
 436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
 437052; AA861697; Hs.120591; ESTs; pros; diag
 437098; N77793; Hs.48659; ESTs; Highly similar to S14458; test; diag
 437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 f; panc, renal; diag
 437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
 437145; AF007216; Hs.5462; solute carrier family 4, sodium; panc, pros, stom; mAb
 437156; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 f; stom, renal, colon; diag
 437181; AI306615; Hs.125343; ESTs; Weekly similar to KAA07; blad; mAb+s.m.

- 437204; AL110216; Hs.359861; ESTs, Weakly similar to I55214; lung; CTL+s.m.
 437212; AI765021; Hs.210775; ESTs; renal, uter, ovar; diag
 437224; AL176228; Hs.97808; ESTs; test; diag
 437259; AI377755; Hs.120695; ESTs; lung; diag
 5 437267; AW511443; Hs.258110; ESTs; BPH; diag
 437289; AA34384; Hs.149420; ESTs; angio; diag
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
 437381; NM_003684; Hs.5591; MAP kinase-interacting serine; glo; CTL+s.m.
 437390; AI125859; Hs.112607; ESTs; lung; diag
 10 437412; BE089288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
 437435; AA249439; Hs.27027; hypothetical protein DKFZp7624; lung; diag
 437437; AA226869; Hs.351823; hypothetical protein DKFZp762L; test; CTL+s.m.
 437476; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.
 15 437553; AI829935; Hs.130497; ESTs, Weakly similar to MATB_H; blad; mAb
 437571; AA760894; Hs.125350; ESTs; pros; diag
 437623; D53880; Hs.5719; chromosome condensation-related; test; diag
 437740; AA810265; Hs.122915; ESTs; mela; diag
 437802; AI476995; Hs.122910; ESTs; panc; diag
 437862; AW978107; Hs.5984; Homo sapiens mRNA; cDNA DKFZp5; mela; CTL+s.m.
 20 437908; AI082424; Hs.351043; ESTs; test; diag
 437915; AI837933; Hs.202312; Homo sapiens clone N11 NTera2D; lung, headnk, ovar, blad, uter; diag
 437931; AI249468; Hs.124434; ESTs; blad; diag
 437936; AW939591; Hs.5840; mucin 13, epithelial membrane; colon, stom, uter, panc; mAb+s.m.
 25 437938; AI950087; Hs.369628; gbwq05c02.x1 NCI_CGAP_Kid12_H; renal, ovar, uter, cerv, blad; diag
 437939; AW298600; Hs.64913; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 437960; AI669586; Hs.369312; ESTs; uter, ovar; diag
 438167; R28353; Hs.24298; chemokine binding protein 2 (C; ovar, breast, uter; mAb
 438199; AW016531; Hs.122147; hypothetical protein FLJ13169; breast; diag
 30 438209; AL120659; Hs.6411; aryl-hydrocarbon receptor nuc; mela; mAb+s.m.
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag
 438274; AI918806; Hs.55080; ESTs; headnk; diag
 438403; AA806607; Hs.292206; ESTs; lung; mAb
 438436; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 35 438450; AI050866; Hs.65853; nodal, mouse, homolog; test; diag
 438456; AA913381; Hs.279763; ESTs; test; diag
 438552; AJ245820; Hs.6314; type I transmembrane receptor ; pros, ovar; diag
 438670; AI275803; Hs.123428; ESTs; fibro; CTL+s.m.
 40 438702; AI879064; Hs.7164; ESTs; lung; diag
 438707; LD8239; Hs.5326; amine acid system N transporter; ovar; mAb
 438746; AI865815; Hs.184727; Human melanoma-associated anti; panc, blad, mela, ovar; mAb+CTL
 438817; AI023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
 438859; AI659626; Hs.33522; Homo sapiens mRNA for KIAA1647; renal; diag
 438866; U44386; Hs.6441; tissue inhibitor of metallopro; mela; diag
 438873; AI032471; Hs.124292; Homo sapiens cDNA: FLJ23123 fl; fibro; diag
 438898; AI819863; Hs.105243; ESTs; lung; diag
 438915; AA280174; Hs.359711; Williams-Beuren syndrome chrom; lung, test, mela; diag
 438929; AW195515; Hs.253177; ESTs; renal; diag
 438958; WI00847; Hs.125056; Human DNA sequence from clone ; lung; diag
 50 438968; AW979074; gb:E8T391184 MAGE sequences; renal; diag
 438983; AF065884; Hs.210229; proacrosin binding protein sp3; test; CTL+s.m.
 438993; AA628995; gb:cd77b08.s1 NCI_CGAP_Ov2 Hom; ovar; mAb+s.m.
 439053; BE244588; Hs.6456; chaperonin containing TCP1, sic; test; diag
 439092; AA830149; gb:cc4f08.s1 NCL_CGAP_GCB1 Hs; pros; diag
 55 439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
 439180; AI593742; Hs.190067; v-erb-A2 avian erythroblastic ; breast, ovar, test, pros, blad, panc, colon, fibro, mela; mAb
 439221; AI737108; Hs.322650; ESTs, Moderately similar to I7; EWS; s.m.
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47592; mela, fibro; diag
 439239; AI031540; Hs.235331; ESTs; blad; diag
 60 439285; AI133916; Hs.478860; hypothetical protein FLJ20083; lung, breast; diag
 439310; AF086120; Hs.102793; ESTs; mela; diag
 439318; AW837046; Hs.6527; G protein-coupled receptor 58; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mela; mAb+s.m.
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretob; fibro, uter, diag
 439386; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
 65 439382; BE247684; Hs.103070; ESTs; angio; diag
 439394; AA149250; Hs.56105; ESTs; lung; diag
 439410; AA632012; Hs.186746; ESTs; angio; diag
 439453; BE264974; Hs.6585; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.
 439498; BE616501; Hs.32343; Homo sapiens. Similar to RIKEN; mela, esoph; diag
 70 439658; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mela, colon; mAb
 439668; AI031277; Hs.302634; fzzed (Drosophila) homolog ; ovar, uter; mAb
 439670; AF086076; Hs.59507; ESTs, Weakly similar to AC01048; lung, headnk, cerv; diag
 439702; AW085525; Hs.55984; ESTs; mela; diag
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAPI_L_H; ovar, lung, headnk; diag
 75 439735; AI635386; Hs.142846; hypothetical protein; pros; diag
 439737; AT751438; Hs.41271; Homo sapiens mRNA full length ; panc; diag
 439750; AI359053; Hs.57694; Homo sapiens mRNA full length ; panc, fibro, breast; diag
 439755; AW749482; Hs.77873; B7 homolog 3; sarc; mAb
 439769; AI359055; Hs.67709; Homo sapiens mRNA full length ; colon, stom, panc, leuk, lung; diag
 439778; AI109729; Hs.99384; putative transmembrane protein; pros; mAb+s.m.
 80 439780; AI109688; gb:Homo sapiens mRNA full leng; blad, esoph; diag
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length ; ovar, uter, cerv, breast, pros ; diag
 439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
 439867; AA847510; Hs.161292; ESTs; panc; diag

439926; H06430; Hs.288433; neurokinin; panc; mAb+diag
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv, diag
 439963; AW247529; Hs.6793; platelet-activating factor ac; breast, lung, blad; s.m.
 5 440042; AI073387; Hs.133898; ESTs; over; CTL+s.m.
 440086; NM_005402; Hs.6906; v-ras simian leukemia viral on; anglo; diag
 440099; AL080058; Hs.6906; DKFZP554G202 protein; panc; diag
 440119; AA865455; Hs.125331; ESTs; Moderatey similar to un; test; diag
 440138; AB033023; Hs.316127; hypothetical protein FLJ10201; lung; CTL+s.m.
 10 440151; AA868167; gbk38e07.s1 Scores_lead.s_NH; sarc; diag
 440207; AI371978; Hs.128326; ESTs; test; diag
 440208; HS05049; Hs.247937; neuredin 3; fibro; diag
 440210; AW674562; Hs.122128; ESTs; glo; diag
 440225; BE295762; Hs.159; tumor necrosis factor receptor; glo; mAb
 15 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
 440266; AI972867; Hs.7130; copine IV; pros; diag
 440273; AI805392; Hs.325335; Homo sapiens cDNA: FLJ23523 f; lung, fibro; diag
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
 440311; AJ733079; Hs.125407; ESTs; Moderatey similar to AL; renal; diag
 20 440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
 440333; AI370424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fs; breast; diag
 440452; AI925136; Hs.56150; ESTs; Weakly similar to CAYP_H; fibro; diag
 440457; BE387553; Hs.21321; Homo sapiens clone FLB9213 PRO; mel; diag
 25 440484; BE328156; Hs.150356; ESTs; panc; diag
 440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 f; pros; diag
 440659; AF134160; Hs.7327; claudin 1; lung; mAb
 440704; M69241; Hs.162; insulin-like growth factor bin; lung, glo, ovar; diag
 440773; AA352702; Hs.37747; Homo sapiens; Similar to RIKEN; test; diag
 30 440801; AA906366; Hs.370308; ESTs; pros; diag
 440819; AI809444; Hs.202108; ESTs; pros; diag
 440901; AA809358; Hs.128812; ESTs; ovar; pros; diag
 440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag
 440983; M20681; Hs.7594; solute carrier family 2 (facil; test; mAb
 441020; WT9283; Hs.36962; ESTs; lung, panc; diag
 35 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
 441065; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fs; panc, cerv, stom, uter, lung; diag
 441134; W29092; Hs.346950; cellular retinoid acid-binding; sarc; diag
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
 441321; H71182; Hs.7771; B-cell associated protein; test; diag
 40 441345; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 441350; AB020890; Hs.7762; paraneoplastic antigen MA2; panc; mAb+CTL
 441377; BE216230; Hs.202656; ESTs; uter, endo, lung; diag
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
 45 441392; AW451631; Hs.222119; ESTs; Weakly similar to S30433; renal; diag
 441457; AW956681; Hs.43698; ESTs; anglo; diag
 441495; AW294603; Hs.127039; ESTs; blad; diag
 441525; AW241867; Hs.127728; ESTs; lung; diag
 441553; AA281219; Hs.121298; ESTs; lung, test, ovar; CTL+s.m.
 50 441633; AW956544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
 441793; AW294903; Hs.132208; ESTs; lung; diag
 441801; AW242799; Hs.86360; ESTs; blad; diag
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
 441859; AW194364; Hs.380444; interleukin-4-induced gene-1 p; ovar, mel; fibro; mAb
 55 441878; AI001889; Hs.127982; ESTs; test; diag
 442006; AW975163; Hs.372210; ESTs; Weakly similar to S72482; fibro, angio; CTL+s.m.
 442082; R41823; Hs.7413; calsyntenin-2; breast, pros, ovar; diag
 442104; L20971; Hs.188; phosphodiesterase 4B, cAMP-spe; anglo; CTL+s.m.
 442108; AW452649; Hs.343259; ESTs; lung; diag
 60 442242; AW647908; Hs.90424; Homo sapiens cDNA: FLJ23286 f; BPH; diag
 442323; AW016669; Hs.29190; ESTs; breast; diag
 442333; AI850877; Hs.129302; ESTs; test; diag
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mel; CTL+s.m.
 65 442438; AA995998; Hs.370007; pbx26b03.s1 NCL_CGAP_Ku5 Hs; uter, ovar, renal; diag
 442441; AI020662; Hs.129598; ESTs; breast; diag
 442503; AI147078; Hs.375091; p53-responsive gene 5; mel; diag
 442506; BE556441; Hs.417226; ESTs; anglo; diag
 442573; H93368; Hs.7587; branched chain amineotransferas; ovar, panc, angio, test; s.m.
 70 442577; AA292995; Hs.163800; ESTs; blad, panc, colon, stom, over; diag
 442580; AI733682; Hs.131238; ESTs; breast ; diag
 442609; AL020596; Hs.8518; selenoprotein N; mel; diag
 442813; AI0004002; Hs.130522; Kv channel-interacting protein; glo; diag
 442622; NM_000435; Hs.8546; Notch (Drosophila) homolog 3; ovar; mAb
 442711; AI161073; Hs.8645; hypothetical protein; angio, mel; sarc; diag
 442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mel; s.m.
 75 442757; AI739528; Hs.28345; ESTs; mel; diag
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 442621; BE391929; Hs.8752; transmembrane protein 4; ovar; diag
 442832; AW205560; Hs.253569; ESTs; pros, fibro; diag
 442898; R37725; Hs.283093; ESTs; panc; diag
 80 442994; AI028718; Hs.16954; ESTs; blad, fibro; diag
 443054; AI745163; Hs.84520; yes-associated protein 85 kDa; blad; diag
 443162; T49951; Hs.9029; DKFZP434G092 protein; blad, lung; CTL+s.m.
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

443184; AB38728; Hs.135169; ESTs; sarc; diag
 443211; AF128386; Hs.143655; ESTs; blad; ovar, lung, headnk, stom, colon; diag
 443216; WB0487; Hs.324521; hypothetical protein DC50; test; diag
 443257; AA334040; Hs.116114; HSPC065 protein; fibro; CTL+s.m.
 5 443400; R28424; Hs.260648; ESTs; lung; diag
 443523; AK001575; Hs.9538; hypothetical protein FLJ10713; test; CTL+s.m.
 443537; DT3305; Hs.203; cholecystokinin B receptor; test; mAb
 443648; AI085377; Hs.143610; ESTs; lung, headnk; diag
 443709; AI082692; Hs.134662; ESTs; fibro; diag
 10 443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
 443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
 443883; AA114212; Hs.9930; serine (or cysteine) proteinases; sarc; s.m.
 15 443885; H91806; Hs.15284; ESTs; mela; diag
 443892; AI889572; Hs.246875; ESTs; lung; diag
 443950; NM_001425; Hs.9939; epithelial membrane protein 3; mela; mAb
 443966; AA287702; Hs.10031; KIAA0355 protein; angio; diag
 443983; H04482; Hs.163724; ESTs; mela; mAb
 20 443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
 444009; AI380792; Hs.136104; ESTs; angio; diag
 444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb
 444159; AF116846; Hs.10431; dead ringer (*Drosophila*)-like ; test; CTL+s.m.
 444163; AI126098; FGENESH predicted RNAseH domain; blad; s.m.
 444301; AK000136; Hs.10760; asporin (LRR class 1); panc; diag
 25 444325; AW152618; Hs.16757; ESTs; esoph; diag
 444330; AI597653; Hs.49265; ESTs; angio; diag
 444342; NM_014398; Hs.10807; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
 44437B; R41339; Hs.47860; neurotrophic tyrosine kinase, ; lung, glio; mAb+s.m.
 444409; AI792140; Hs.49265; ESTs; angio; diag
 30 444444; AI149332; Hs.14855; ESTs; blad; diag
 444471; AB020584; Hs.11217; KIAA0877 protein; glio, lung, colon ; mAb
 444478; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA; blad; s.m.
 444484; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 444633; AF111713; Hs.12224; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
 35 444649; AW207523; Hs.371001; ESTs; blad; diag
 444670; H68373; Hs.332938; hypothetical protein MGC6370; sarc; diag
 444754; T03911; Hs.11881; transmembrane 4 superfamily me; panc, amuc, stom, lung, colon; mAb+s.m.
 444809; BE207568; Hs.208219; oculospanin; mela; mAb
 444823; BE252989; Hs.12045; putative protein; test; diag
 40 444853; AW384082; Hs.104879; serine (or cysteine) proteinases; mela; s.m.
 444895; AN674383; Hs.22894; sttute carrier family 7 (carb); ovar; mAb+s.m.
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
 445019; AI205540; Hs.281285; ESTs; headnk, lung, colon; diag
 445070; NM_000677; Hs.256; adenosine A3 receptor; glio, renal; mAb
 446076; AI206888; Hs.154131; ESTs; test; diag
 445084; H38914; Hs.260848; hypothetical protein FLJ14761; sarc; mAb
 445093; AI207197; Hs.156905; ESTs; test; diag
 445109; AF039916; Hs.12330; deoxyribonucleoside triphosphate dt; pros; s.m.
 50 445118; AF035121; Hs.12337; kinase insert domain receptor ; angio; mAb
 445160; AI299144; Hs.101937; she oculis homeobox (*Drosophila*; sarc; CTL+s.m.
 445182; AW189787; Hs.361773; ESTs; blad; diag
 446247; AW274250; Hs.153997; ESTs; mela; diag
 445279; R41800; Hs.22245; ESTs; angio; diag
 55 445303; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
 445413; AA151342; Hs.12677; CG147 protein; pros, colon, uter, ovar, lung, panc; diag
 445418; AW139377; Hs.127179; cryptic gene; panc; diag
 445424; AB028945; Hs.12696; contactin SH3 domain-binding p; pros ; diag
 445443; AV653838; Hs.295131; ESTs; lung; diag
 60 445654; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
 445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
 445784; AI253159; Hs.146065; ESTs; mela; CTL+s.m.
 445885; AI734009; Hs.127689; KIAA1603 protein; pros, fibro; diag
 65 445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA ; renal, leuk; mAb
 445911; AI985987; Hs.145645; ESTs; Moderately similar to Al; blad; diag
 445982; BE410233; Hs.13501; pescadillo (zebrafish) homolog; mela; diag
 446057; AI420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb
 446082; AI274138; Hs.156452; ESTs; blad; diag
 70 446098; AW072216; Hs.208470; ESTs; angio; diag
 446100; AW987109; Hs.19804; hypothetical protein dj462023; pros; diag
 446102; AW168057; Hs.317694; ESTs; lung; diag
 446113; AW987533; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
 75 446291; BE397763; Hs.14622; Interferon, gamma-inducible pr; mela; diag
 446292; AF081497; Hs.279682; Rb type C glycoprotein; lung, cerv; mAb
 446293; AI420213; Hs.149722; LIM domain transcription factor; ovar, test; diag
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase ; pros; s.m.
 446332; AK001635; Hs.14836; hypothetical protein FLJ10773; breast; diag
 446342; BE298665; Hs.14846; solute carrier family 7 (carb); uter, colon, pros, mela; mAb
 446422; AW082270; Hs.12496; ESTs; Weakly similar to ALU4_H; fibro; diag
 80 446529; AI076640; Hs.15249; nucleolar protein 1 (120kD); lung, test; diag
 446608; N75217; Hs.175622; ESTs; uter, fibro; diag
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
 446644; NM_003272; Hs.21065; transmembrane 7 superfamily mem; mela; mAb
 446673; NM_016361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag
 446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
 5 446733; AA863360; Hs.20040; ESTs; Weakly similar to fatty ; breast; s.m.
 446755; AW451473; Hs.16134; serina/threonine kinase 10; mela; CTL+s.m.
 446791; AI632276; Hs.195922; ESTs; test; diag
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
 10 446856; AI814373; Hs.164175; ESTs; lung; diag
 446868; AV660737; Hs.346297; ESTs; panc; diag
 446872; X9705B; Hs.16362; pyrimidinergic receptor P2Y; G; lung; mAb
 446832; AA861459; Hs.125644; ESTs; fibro; diag
 446957; AI699829; Hs.156781; ESTs; fibro; diag
 446979; AI654433; Hs.197683; ESTs; test; diag
 15 446984; AB020723; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.
 446989; AK001698; Hs.16740; hypothetical protein FLJ11036; lung, headnk; diag
 446990; NM0013; Hs.27896; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
 446999; AA151520; Hs.351418; hypothetical protein MGCG4485; headnk; diag
 20 447004; AW296986; Hs.157539; FGENESH predicted secreted pro; glo; diag
 447076; AW885727; Hs.9914; ESTs; lung; diag
 447126; AW150632; Hs.170307; Rat guanine nucleotide exchang; angio; diag
 447164; AF026941; Hs.17518; vimentin similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
 447178; AW594641; Hs.192417; ESTs; mela; diag
 25 447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag
 447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.
 447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
 447334; AA516032; Hs.91109; ESTs; blad; diag
 447343; AA258841; Hs.236894; ESTs; Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
 30 447350; AI375572; Hs.172634; v-ab-a avian erythroblastic 1; breast, ovar, uter; diag
 447377; X77343; transcription factor AP-2 alpha; breast, lung, mela; CTL+s.m.
 447395; AI418412; Hs.164793; Homo sapiens cDNA: FLJ21810 fi; panc; diag
 447437; U07225; Hs.339; purinergic receptor P2Y; G-pro; blad; mAb
 447499; AW262580; Hs.147674; protocadherin beta 16; pros, glo, ovar ; mAb+s.m.
 35 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
 447534; AW953935; Hs.268655; ESTs; lung, test; diag
 447578; AA912347; Hs.136585; ESTs; Weakly similar to JC6314; ovar; s.m.
 447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 447604; AW089933; Hs.301342; hypothetical protein MGCG4342; mela; diag
 447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.
 40 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
 447748; T53280; Hs.32297; ESTs; renal; diag
 447761; AF061573; Hs.19492; protocadherin 8; EWS, glo; mAb
 447768; X86400; Hs.19520; FXYD domain-containing ion tra; renal; mAb
 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA; renal; diag
 447835; AW591623; Hs.164129; ESTs; Weakly similar to I38022; renal, ovar, uter; diag
 447881; BE620880; Hs.355279; GCN1 (general control of amino; renal; diag
 447937; AL109716; Hs.201034; Homo sapiens mRNA full length ; mela; mAb
 447983; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 50 448030; NM0714; Hs.328950; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb
 448045; AJ297436; Hs.20168; prostate stem cell antigen; blad, panc, pros; mAb
 448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
 448133; AA723157; Hs.37769; folate receptor 1 (adult); ovar, fibro; mAb
 448140; AF146761; Hs.20490; BCM-like membrane protein prec; fibro, mela, leuk; mAb
 55 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase; test; CTL+s.m.
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
 448204; AI475124; Hs.170561; ESTs; sacr; diag
 448231; AJ701916; Hs.202509; ESTs; angio; diag
 448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
 448262; AW880830; Hs.186273; ESTs; blad; diag
 60 448275; BE514434; Hs.20830; kinase-like 2; ovar, esoph, mela; diag
 448278; W07369; Hs.11782; ESTs; lung; diag
 448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 fi; pros; diag
 448321; NM_005683; Hs.20912; adenomatous polyposis coli like; glo; CTL+s.m.
 65 448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag
 448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
 448437; AW470125; Hs.220529; gbxw60c04_x1_NCL_CGAP_Pan1 Ho; panc, colon; diag
 448499; BE613280; Hs.77550; p53-regulated DDA3; glo; diag
 448509; BE382657; Hs.21406; signal transducer and activate; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.
 70 448558; AI970276; Hs.156905; KIAA1676; test; CTL+s.m.
 448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glo; mAb
 448664; AB79317; Hs.334651; splicing factor 3a, subunit 1; mela; CTL+s.m.
 448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag
 448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
 75 448706; AW291095; Hs.21814; interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
 448719; AA023627; Hs.21850; triunucleotide repeat containin; mela, sacr; CTL+diag
 448776; AB025237; Hs.388; nudix (nucleoside diphosphate ; test; diag
 448811; AI590371; Hs.199460; ESTs; esoph, panc; mAb
 448939; BE267795; Hs.22596; hypothetical protein FLJ10637; test; CTL+s.m.
 80 448966; AW372914; Hs.88149; phosphoinositol 3-phosphate bi; mela; CTL+s.m.
 448981; AI968719; Hs.195387; ESTs; test; diag
 448980; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
 448993; AI471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
 448999; AF179274; Hs.22794; transmembrane protein with EGF; pros, glo ; mAb

449003; X76342; Hs.389; alcohol dehydrogenase 7 (class; lung, headnk; s.m.
 449019; A1949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.
 449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
 449076; AK001256; Hs.22975; KIAA1576 protein; melu; diag
 449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
 449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7_J; sarc; diag
 449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
 449207; AL044222; Hs.23255; nucleoporin f155kD; lung; diag
 10 449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag
 449230; BE513348; Hs.356392; melanoma cell adhesion molecule; lung, cerv, headnk, blad, ovar, colon; mAb
 449317; AW293413; Hs.132906; 19A24 protein; melu; mAb
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, anglo; CTL+s.m.
 15 449322; AI638616; Hs.196566; ESTs; test; diag
 449338; H73444; Hs.394; adrenomedullin; renal; diag
 449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 f16; anglo; mAb
 449437; AT702038; Hs.100057; Homo sapiens cDNA FLJ22902 f1; test; diag
 449446; D607030; Hs.57471; ESTs; blad, lung, headnk, breast; diag
 449467; AW205008; Hs.197042; ESTs; lung; diag
 20 449494; AW237014; Hs.315369; aquaporin 4; fibro; diag
 449568; AI655634; Hs.195389; ESTs; test; diag
 449592; AI655494; Hs.195718; ESTs; panc; diag
 449618; AI075450; Hs.15978; KIAA1272 protein; anglo; diag
 25 449625; NM_014263; Hs.349094; cdz (odd Ozfem-m, Drosophila); pros; diag
 449650; AF055575; Hs.23888; calcium channel, voltage-dependent; pros; mAb
 449680; AI033621; Hs.12160; ESTs; renal; diag
 449981; AW265634; Hs.131100; ESTs; glio, esoph, lung, blad; diag
 449976; HO8360; Hs.135056; Human DNA sequence from clone ; lung; diag
 30 450096; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter, diag
 450148; AW989781; Hs.132863; Zic family member 2 (odd-paire; sarc; CTL+s.m.
 450152; AI138635; Hs.22968; Intron of VEGFR; renal; diag
 450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag
 35 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 f15; pros; diag
 450400; AI694722; Hs.279744; ESTs; panc; diag
 450431; AW136797; Hs.266041; ESTs; test; diag
 450451; AW591528; Hs.202072; ESTs; uter, endo; diag
 450506; NM_004460; Hs.416; fibroblast activation protein; panc, esoph; diag
 450534; AI570189; Hs.25132; KIAA0470 gene product; anglo; CTL+s.m.
 40 450588; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
 450638; AW403954; Hs.25227; mesenchymal stem cell protein ; blad; mAb
 450642; R28773; Hs.7130; copine IV; pros; diag
 450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
 450663; H43640; Hs.25292; ribonuclease HI, large subunit; melu; s.m.
 450676; AI147155; Hs.279727; ESTs; sarc; diag
 450684; AA872805; Hs.25333; Interleukin 1 receptor, type I; blad, lung, headnk; mAb
 450690; AA296696; Hs.333418; FXVY domain-containing ion tra; melu; diag
 450693; AW490461; Hs.203965; ESTs; pros, uter; diag
 450719; AI095837; Hs.21349; ESTs, Weakly similar to RB8B_H; test; diag
 50 450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 450785; AA852713; Hs.108895; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 450832; AW970602; Hs.105421; ESTs; lung; diag
 451027; AW619204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag
 55 451035; AU076785; Hs.430; plasmin 1 (f zefurin); panc; diag
 451050; AW937420; Hs.351868; ESTs; melu; diag
 451089; R52795; Hs.25954; interleukin 13 receptor, alpha; glio, fibro, melu; mAb
 451108; BE382701; Hs.25980; N-MYC oncogene; test, ovar; CTL+s.m.
 451110; AR955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
 451181; AT796330; Hs.207461; ESTs; panc; diag
 60 451253; HA6239; Hs.26126; claudin 10; lung, ovar, panc; mAb
 451291; R39288; Hs.5702; ESTs; lung; diag
 451295; AI557212; Hs.17132; ESTs, Moderately similar to l5; panc; diag
 451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1; lung; s.m.
 451346; NM_005338; Hs.26312; gliome amplified on chromosome; ovar; mAb
 451386; AB029006; Hs.26334; specific paraplegia 4 (autosome; lung; diag
 451398; AT793124; Hs.144479; ESTs; breast, ovar; diag
 451411; AA017492; Hs.135655; ESTs; pros; diag
 451497; HB3294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
 451541; BE278303; Hs.26557; plakophilin 3; lung, blad, ovar; diag
 70 451592; AB055416; Hs.213897; ESTs; lung, headnk; diag
 451635; AA018892; Hs.127179; cryptic gene; panc; diag
 451663; AB72360; Hs.202983; ESTs; pros; diag
 451720; AW970985; Hs.290853; ESTs; pros; diag
 451749; AW074260; Hs.336428; ESTs; lung; diag
 451820; AW058357; Hs.193240; ESTs; panc; mAb
 451844; T61430; glycogen603.61 Strategus; lung ; blad; diag
 451952; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb
 451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/Hs) b; test; CTL+s.m.
 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
 80 452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag
 452240; AI591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
 452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 452244; N33530; Hs.176674; ESTs; melu; diag

452291; AF015592; Hs.26853; CDC7 (cell division cycle 7, S; test; CTL+s.m.
 452295; BE379936; Hs.28866; programmed cell death 10; lung; diag
 452298; AI039243; Hs.278585; ESTs; angi; diag
 5 452304; AA025306; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
 452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc; pros; CTL+s.m.
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb
 10 452367; U71207; Hs.29279; eyes absent (*Drosophila*) homolog; lung, pros, over, liver; CTL+s.m.
 452418; AA026115; Hs.114777; ESTs; fibro; diag
 452461; NT8223; Hs.100103; transcription factor; blad, lung, headnk, over, glio, stom, colon, cerv; CTL+s.m.
 452571; W31518; Hs.34655; ESTs; stom, lung, panc, colon, fibro; diag
 452594; AU076405; Hs.29981; solute carrier family 26 (sulf); over; mAb
 15 452613; AA481599; Hs.23459; ESTs; lung; diag
 452679; Z42387; Hs.03883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
 452705; H48805; Hs.246005; ESTs; panc; diag
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag
 452721; AJ269529; Hs.301871; solute carrier family 37 (glyc); pros; mAb
 20 452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE3535; blad; diag
 452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; mela; diag
 452792; AB037765; Hs.30652; KIAA1344 protein; pros, over, breast; diag
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
 25 452833; BE559681; Hs.30736; KIAA0124 protein; lung, mela; CTL+s.m.
 452865; AJ024046; Hs.119567; ESTs, Weakly similar to A47682; lung; diag
 452899; M95739; Hs.30956; nescient helix loop helix 1; sac; CTL+s.m.
 452924; AW580839; Hs.97199; complement component C1q recep; angio; diag
 452933; AW391423; Hs.288555; Homo sapiens cDNA: FLJ22425 f; angio; CTL+s.m.
 30 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.
 453006; AI362575; Hs.303171; ESTs; pros; diag
 453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.
 453085; AW854243; Hs.351573; KIAA0251 protein; angio; diag
 453096; AW294631; Hs.351270; ESTs; pros; diag
 35 453102; NM_007197; Hs.31664; frizzled (*Drosophila*) homolog ; lung, headnk, colon; mAb
 453107; NM_016113; Hs.279746; vanilloid receptor-like prot; mela; mAb
 453134; AA032211; Hs.118493; ESTs; blad; diag
 453142; AA033546; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
 40 453160; AI263307; Hs.356904; H2B histone family, member 1; lung, panc, pros; diag
 453210; AL133161; Hs.32360; hypothetical protein FLJ10067; lung; CTL+s.m.
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
 453258; AB55587; Hs.32556; KIAA0379 protein; mela; diag
 453310; X70097; Hs.553; solute carrier family 8 (neuro); fibro; mAb
 453321; AB984381; Hs.232521; ESTs; blad; diag
 453323; AF034102; Hs.32951; solute carrier family 29 (nuc); over; CTL+s.m.
 453331; AI240865; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
 453344; BE349075; Hs.44571; ESTs; mela; diag
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
 453385; AA035211; Hs.17404; SOX7 SRY (sex determining regt); angio, blad; CTL+s.m.
 50 453370; AI470523; Hs.139396; ATP-binding cassette, sub-fam; pros; mAb
 453389; BE273548; Hs.32953; cadherin 6, type 2, K-cadherin; renal, over, blad; mAb+s.m.
 453392; U23752; Hs.32954; SRY (sex determining region Y); over, lung, glio, sac; CTL+s.m.
 453459; BE047032; Hs.257789; ESTs; over, cerv, blad, uter, panc, angio, lung; diag
 453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb
 55 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag
 453637; NM_002589; Hs.34073; BH-prostaglandin (brain-heart); headnk; mAb
 453642; AI370936; Hs.34074; dipeptidylpeptidase VI; glio; mAb
 453770; N5187; Hs.43398; 28kD interferon responsive pro; mela; diag
 453789; AA628517; Hs.118502; ESTs; angio; diag
 60 453857; AL080235; Hs.35861; Ras-induced senescence 1 (FLI81; glio, lung, over, headnk, cerv, panc, pros, sac; mAb
 453883; AI638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
 453884; AA355925; Hs.36232; KIAA0185 gene product; lung, over, test, esoph; diag
 453912; AI121034; Hs.356843; SW/SNF related, matrix assoc; mela; diag
 65 453922; AF053306; Hs.35708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.
 453935; AI633770; Hs.42572; ESTs; panc; diag
 453941; U93817; Hs.368820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
 453964; AI961496; Hs.249198; ESTs; lung; diag
 453966; BE149734; Hs.63325; transmembrane protease, serine; colon, blad, lung, over, panc, headnk; mAb+diag+s.m.
 70 453985; N44545; Hs.251865; ESTs; test; diag
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 fam; lung, headnk; s.m.
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
 454066; X00358; Hs.37056; calcitonin/calcitonin-related ; lung; diag
 454071; AI041793; Hs.42502; ESTs; breast; diag
 454077; AC005952; Hs.37052; insulin-like 3 (Leydig cell); test; diag
 75 454098; W27953; Hs.217493; Pleckstrin; lung; diag
 454117; BE410100; Hs.40368; adaptor-related protein comple; mela; CTL+s.m.
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fam; glio; mAb
 454428; BE273437; Hs.301406; hypothetical protein PP3501; mela; mAb
 454438; AW819152; Hs.1544320; DKFZP588O1646 protein; lung; diag
 80 454478; AW805749; Hs.372783; superoxide dismutase 2, mboch; mela; s.m.
 455601; AI368680; Hs.818; SRY (sex determining region Y); lung, cerv, esoph; s.m.
 456034; AW450979; gb:U-H-BK3-ata-a-12-0-U1 N; blad, fibro; diag
 456052; AI666286; Hs.71952; ESTs, Weakly similar to B35298; fibro, ovar, uterus; diag

456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag
 456266; L29073; Hs.198726; cold shock domain protein A; pancreas; CTL+s.m.
 456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL
 5 AA721325; Hs.169058; ESTs, Highly similar to Sim1a; pancreas; diag
 456723; 243902; Hs.4748; adenylyl cyclase activating polypeptide; glio; mAb+s.m.
 456736; AW248217; Hs.1619; actin-binding protein complex (Drosophila); lung; diag
 456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio, lung; mAb
 456B47; AI360456; Hs.86088; ESTs; test; diag
 456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.
 10 456977; AK000252; Hs.168758; hypothetical protein FLJ20245; angiogenesis; diag
 457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.
 457211; AW972565; Hs.32399; ESTs, Weakly similar to Ss1797; melia, pros; CTL+s.m.
 15 457292; AI921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb
 457313; AF047002; Hs.241520; hypothetical protein coactivator; test; CTL+s.m.
 457411; AW085861; Hs.130093; iroquois-class homeobox protein; breast, fibro; diag
 457465; AW301344; Hs.122908; DNA replication factor; test, melia; diag
 457498; AI732230; Hs.191737; ESTs; pros; diag
 457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb
 20 457590; AI612809; Hs.5378; hypothetical protein MGC10724; ovary; diag
 457869; AI077186; Hs.108685; Homo sapiens, alpha-1 (VI) collagen; sarc; CTL+s.m.
 458092; W67353; Hs.360558; KIAA0251 protein; lung; diag
 458124; AW005548; Hs.124590; ESTs; fibro; diag
 458435; AI418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag
 458471; AW648609; Hs.194240; ESTs; renal, panc, hepC; diag
 25 458933; AI638429; Hs.24763; RAN binding protein 1; lung, test; diag
 459373; BE408286; Hs.301408; hypothetical protein PP3501; melia; mAb
 459576; AW612530; Hs.304491; EST; melia; diag
 459702; AI204995; gican03c03_x1 Stratagene schiz; blad, fibro; diag
 30 459705; BE082764; Hs.270262; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
35	Pkey	CAT Number	Accession
40	103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075778 AA075221 AA076395 AA6650486 AA083500
	108202	108971_1	AA065143 AA065142
	113230	2327174_1	AI620548 AI621336 T61430
	118417	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI618326 AF080230 AI63034 AI63036 AI665466 BF512210 U87595 U87599 BE650633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 Hs9001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92279 N66048 BE219539 BE671665 AI624817 BE466111 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF082180 BE466420 AI887798 BF874385 AA204735 AW496808 AA204833 AA207155 BI004755 AA206262 AI365204 H77608 AW590511
45	121335	1369289_1	AA404418 AJ217248
	126872	685588_1	AA136653 AA136656 AW450979 AA984368 AA809054 AW238038 AA492073 BE168945
	322521	14637_1	AF147347 T55503 T55426
	322975	1784158_1	C16391 C16413
	323332	245301_1	AI829520 AJ791892 AJ791823 AA229315 AA228414 AA229211
	323817	887879_1	AA410943 BF366582 AA334202 AA332882 BF371899 AW948863
	324261	1026976_1	AI044891 AI908240 AA393080 AW748403 BE063341 BF330573
	406685	0_0	M18728
55	409051	107934_1	AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083B21 AA062836 AA113B92 AA076318 AA076594 AA078900 AA134801 AA063293 AA083403 AW974305
	409123	108378_1	AA070050 AA070823 AA063403
	409745	MH1044_5	BK030979 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 AA027884 BI009100 BI0085275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762
60	411880	1139083_1	BE086101 T05990 AW872477
	413804	1556661_1	BE168256 BE168190 T646982
	414221	685588_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	417886	1031334_1	AA210987 D57284 AA214584 AA207006 D56572
	427260	11272_50	AA401424 AA001000 AA663848
	427298	115241_1	AA83717 BF061897 AW628327 AA641788 AA400495
	427521	513212_1	AW973352 BF222829 AW016853 BF059130 AI561829 BE6561767 AA568414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206185
	428163	1238297_1	AA548736 AA766578 AI539081 AW029587 AA736837 N79575 AW594357 AA480892
	432189	112710_1	AW874271 AA592975 AA447312 AA884768
	432222	539529_1	AA527941 AA636266 AI610608 AI620190
	432407	MH1429_12	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
75	432415	11371_1	BG036675 BF772005 BF771866 BG060386 BG903081 NM_005712 AF110317 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW874519 AA099426 AW817881 AW856386 BG061122 AA224498 AA308542 AW821833 BF902156 AI732411 BG778834 BG283841 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 E861466 AA663341 AA457591 BG649294 AW392888 AA071122 AA227849 AA584918 BG059570 BF773486 AL041698 BF955013 R87170 C168593 BF770411 BE771288 AI075321 L13823 AA216700 BF771864 AW851859 BE537068 C18995 AA155719 BF771172 BF789107 BF804984 AW818172 AW818143 AW392930 AW817057 AW853044 BF746211 AA17992B AW881687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA065592
80	434414	35978_1	BG166382 AW161066 N42363 BE935013 BE934993 BG291451 AW700520 BG152773 AI224956 AI079625 AW054705 AA843979 AI744193 F04060 T23457 F04044 AA723859 AA977643 AA283764 AI123609 N21561 BF050502 BE856661 AI804220 AA843394 AI472045 AI740490 AA578830 H09495 AI283334 AA609495 AI122773 AW162643 AW161798 BF940077 AI808825 AI60866 AI123189 RA0236 R20728 AW975899 BE764052 N31709 N31708 AI031947 AW194138
			AF134164 BF809407 AA218567 BF842863 AI287168 BF876178 BG999259 AW861851 AW858362 AI817546 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871064 BE001132 BF826831 AW754298

AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950266 AI829309 BG987850 BE093175
BF854337

	434596	14701_1	AF147374 T59538 T59569 T59598 T59542
	434609	14739_1	AF147390 R76593 R76594
5	438966	1242593_1	AW979074 AA834841 AA828650
	439993	2580163_1	AI826361 AA834879 AA828695
	439092	919640_1	AW978407 AA830149 MB5989 AW503637 BF352096
	439780	49082_1	AL109688 R23665 R26578
10	440151	1879911_1	AA868167 F21558 F31418 F35624
	444163	682245_1	BG403189 AI148521 AI184746 AI126098 RD5933 BI057330
	451844	2327174_1	AI820546 AI821336 T61430
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW968908 AA528756 AW440776 BI044354

15 TABLE 3C

Pkey: Unique number corresponding to an Eos probeset.
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

20 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
25	325372	5866020	Minus	1117061-1117304
	325544	6682452	Plus	171228-171286
	327036	6531965	Plus	319951-320040
	327075	6531965	Plus	4041318-4041431
30	327414	5867760	Plus	102481-102586
	328700	5868264	Plus	764089-764203
	330211	6013692	Plus	59158-69215
	332798	Dunham, I. et al.	Minus	232147-231974
	333769	Dunham, I. et al.	Plus	7695625-7695707
35	333904	Dunham, I. et al.	Minus	8217374-8217261
	334223	Dunham, I. et al.	Minus	12734365-12734269
	334447	Dunham, I. et al.	Plus	14308764-14308824
	335115	Dunham, I. et al.	Minus	21386250-21388146
	335809	Dunham, I. et al.	Plus	26310772-26310909
40	335824	Dunham, I. et al.	Plus	26376860-26376942
	335825	Dunham, I. et al.	Plus	26378175-26378268
	335936	Dunham, I. et al.	Minus	27360474-27360400
	336034	Dunham, I. et al.	Plus	29014404-29014590
	336152	Dunham, I. et al.	Minus	30156053-30155870
45	336636	Dunham, I. et al.	Plus	988418-989185
	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338159	Dunham, I. et al.	Minus	11794465-11794943
	338255	Dunham, I. et al.	Minus	16242294-15242231
	400494	9714719	Plus	169845-170272
50	400517	9796606	Minus	49996-50346
	400651	8117978	Minus	81488-81646
	400655	8118496	Plus	16879-17023
	400773	8131629	Minus	44116-44238,48208-48321
55	400844	9188605	Plus	24745-24872,26035-25204
	400846	9188605	Plus	39310-39474
	400881	2842777	Minus	91446-91609,92123-92265
	401093	8516137	Minus	22335-23165
	401234	9929642	Plus	120173-120337
	401424	8176894	Plus	24223-24428
60	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
	401704	3097841	Plus	24712-25374
	401732	1200312	Plus	19346-19525,19625-19708,19887-19973,2006
	401747	9789672	Minus	118596-118816,119119-119244,119609-11978
65	401760	9929699	Plus	83126-83280,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29295,2941
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401785	7249190	Minus	165776-168986,168189-168314,166408-16656
	401797	6730720	Plus	6973-7118
70	401894	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	402145	8018280	Plus	113088-114800
	402199	8576118	Minus	84187-84744
	402230	9866312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
75	402260	3399665	Minus	113765-113910,115853-115765,116808-11694
	402265	3287673	Plus	21069-21168
	402305	7328724	Plus	40632-41362
	402420	9796339	Plus	129750-129919
	402424	9796344	Minus	64925-65073
80	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	402474	7547175	Minus	53526-53628,65755-65920,57530-57757
	402550	7652009	Minus	80413-80573
	402604	9909420	Plus	20393-20767
	402605	9909420	Minus	47680-47973

	402606	8909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
5	402777	9588235	Plus	126786-126948
	402860	9588237	Minus	76423-76560
	402888	9930892	Minus	54727-54801
	402892	7767907	Minus	42137-42515
	402894	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137095
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
15	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
20	403745	7239669	Plus	85128-85292
	403740	7630882	Plus	86504-87227
	403776	7770511	Minus	1414-1513,1624-1756
	403903	7710571	Minus	101165-102597
	404029	7671252	Plus	109716-111112
25	404049	3688074	Minus	75765-78155
	404210	5006246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404263	9367202	Minus	56575-56055
	404286	2326614	Plus	51086-51301
30	404298	8944263	Minus	73591-73723
	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404686	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68690-69563
	404998	6007890	Plus	37999-38145,38852-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	406238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144454,144690-144836,151750-15188
	405451	7622617	Minus	145349-146227
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
45	405547	1054740	Plus	124361-124520,124914-125050
	406646	4914350	Plus	741-969
	405704	4204244	Plus	138842-139061
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405932	7707812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71754-71944
55	406360	9256107	Minus	7813-7873
	406399	9256288	Minus	63448-63554
	406434	9266661	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-6877
60	406547	7711513	Minus	172780-174368

Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59681 probesets on the Affymetrix/Eco-Hu3 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

75	Pkey:	Unique Ecs probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	Unigene number
	Pred.Prot.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
80	UniGene Title:	Unigene gene title
	R1:	Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Pkey ExAccn UniGeneID Pred.Prot.Domains UniGeneTitle R1

				TM=M;SS=M		
4	419551	AW582256	Hs.91011		anterior gradient 2 (Xenopus laevis	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinorhin	7.0
	409340	BE174629	Hs.321130	aa_permeases_pyridoxal_da	melanophillin (MLPH), mRNA	6.8
5	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	strafin	6.4
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	trefoil factor 3 (intestinal)	6.3
	447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, weakly similar to Homolog of	6.1
	406367			Target Exon	Target Exon	6.0
10	421814	L12350	Hs.108623	EGF_tsp_1,vwc,TSPN,tsp_3;	thrombospondin 2	5.8
	406867	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	kerafin 19	5.8
	426104	A204418	Hs.190080		ESTs	5.8
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
15	426539	AB011155	Hs.170290	SH3_PDZ_Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXYD domain-containing ion transp	5.5
	419329	AY072220	Hs.289998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
	418344	AA216387			g0nc16b02s1 NCL_CGAP_Pr1 Homo sap	5.2
	407116	AA130986	Hs.271627		ESTs	5.1
	417369	BE260984	Hs.82045	PTN_MK;TM=M;SS=Y	midline (neurite growth-promoting f	5.1
20	419452	U33635	Hs.90572	Ig_pknaase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026692	Hs.105700	Fz_NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
	408453	AB855518	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	WT4001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
25	417515	L24203	Hs.82237	zf_B_box,zf_UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide 3-kinase, regulato	5.0
	422087	X58968	Hs.111301	fm2_hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	Ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily contain	4.9
	408491	AU08B063	Hs.7882		ESTs	4.9
30	417944	AU077196	Hs.82985	vwc,Collagen,COLIFI;TM=N;S	collagen, type V, alpha 2	4.9
	408062	AL157486	Hs.50150	hemopexin;TM=N;SS=M	Homo sapiens mRNA; cDNA DKFZp564B18	4.9
	422281	M35803	Hs.346935	Ig_kringle,pknaase,F2;TM=	hemopexin	4.9
	425308	M07639	Hs.155585	homeobox;TM=M;SS=N	receptor tyrosine kinase-like orpha	4.8
35	408349	BE546947	Hs.44276		homeo box C10	4.8
	449019	AA949995	Hs.87776	MAGE_Cys_Jonot,EGF_Jaminin	ESTs, weakly similar to T22341 hypo	4.8
	435561	AA351978	Hs.4943	Ig_kringle,pknaase,F2;TM=	hepatocellular carcinoma associated	4.8
	410687	U24389	Hs.65436	Ly6L_oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
	429455	AA472111	Hs.278694	Icacin_c	CD209 antigen	4.8
	414407	AA147026	Hs.76704		EBTs	4.8
40	419390	AT011862	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGCI1138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
	411089	AA445454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
	450172	NM_005864	HE24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
45	449717	AB040935	Hs.23954	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	AA177901	Hs.208641	actin,none	ESTs	4.6
	435370	AA984074	Hs.226838	EGF_fn3_ibrinogen_C,tox	ESTs	4.6
	411761	AT733848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	AJ243706	Hs.143323	PHD_ARID_jmJC_jmJN_zf-CSH	putative DNA/chromatin binding moti	4.6
50	426935	NM_000888	Hs.172928	vwc,Collagen,COLIFI;TM=M;S	collagen, type I, alpha 1	4.5
	408796	AA688292	Hs.170345	hormone_rec_zf-C4	ESTs	4.5
	407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
	422830	AC007954	Hs.121971		hypothetical protein DKFZp434P0111	4.4
	447528	AI812027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGCI9381, mRNA,	4.4
55	430168	AW8668343	Hs.145582	efhand,efhand	DKFZP434I1735 protein	4.4
	432225	AA852004	Hs.125339	AA_Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156542	Hs.72127	homeobox,HLH	ESTs	4.4
	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
	444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
60	453957	AL080236	Hs.35861	TM=Y;SS=M	Ras-induced senescence 1 (RS1)	4.4
	413859	AW992355	Hs.8364	SAM_PNT,none	Homo sapiens, pyruvate dehydrogenase	4.3
	440369	AW170150	Hs.132449	TM=M;SS=M	downstream of breast cancer antigen	4.3
	418140	BE513836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
	441384	AA447849	Hs.288680	7tm_3,none	retinoic acid induced 3	4.3
65	424464	R68537	Hs.17952	homeobox,none	ESTs	4.3
	423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fs, clo	4.3
	432562	BE531048	Hs.276742	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
	433320	D60647	Hs.250879	rrm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW000888	Hs.118268		prostate cancer associated protein	4.2
	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
70	448913	AA194422	Hs.22564	rrm,z-RanBP,phnase,GST_-	myoain VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
	400496			TM=Y;SS=N	ENSP0000224716*GTP-binding proti	4.2
	442599	AF078037	Hs.324051	SH3_ank;TM=M;SS=N	RelA-associated inhibitor	4.2
	448520	AB002367	Hs.21355	pknase,DCX;TM=M;SS=N	doublecordon and Cam kinase-like 1	4.2
75	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to I38122 hypo	4.2
	428485	NM_006207	Hs.170940	IgTM=NCSS=M	platelet-derived growth factor rece	4.2
	435558	AF254260	Hs.283009	bZIP;TM=M;SS=N	tutelin 1	4.2
	446051	BE048061	Hs.37054	Ephrin_A_deamln_dsmn,z-el	ephrin-A3	4.2
	451982	F19036	Hs.27373	NNNA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa_integrin_A_FG-GAP;TM=	integrin, alpha 2 (CD49b, alpha 2 s	4.1
	434449	AW953484	Hs.3849	efhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rec;TM=M;SS=N	em1 sequence (mammary tumor and sq	4.1

	423057	AW961597	Hs.130816		ESTs, Moderately similar to I38022	4.1
	452063	R53185	Hs.32366	HJH;TM=M;SS=N	ESTs, Weakly similar to TWST_HUMAN	4.1
	450680	AF131784	Hs.25318	nts,none	Homo sapiens clone 25194 mRNA sequa	4.1
	416283	S79895	Hs.83942	Peptidase_C1;TM=N;SS=M	calhepsin K (pneyodysosis)	4.1
5	416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262630	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.184101	7m_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted figand homologous	4.1
10	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	425272	AI01922	Hs.135121	HSPT0	hypothetical protein FLJ22415	4.0
	448828	AI580252	Hs.255565	TM=N;SS=M	ESTs, Weakly similar to putative p1	4.0
	419648	T73651	Hs.91877	TM=Y;SS=M	thyroid hormone responsive SPOT14 (4.0
15	421485	AA243499	Hs.104800		hypothetical protein FLJ10134	4.0
	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
	417363	AW129357	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
20	452239	AW379378	Hs.356269		protein tyrosine phosphatase, recep	4.0
	444286	AI625304	Hs.201088		ESTs	4.0
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
	451304	M92642	Hs.26208	Collagen, TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
	441094	U33819	Hs.7647	zf-C2H2_LJM,PHD,TFIIS;TM=	MYC-associated zinc finger protein	4.0
25	407788	BE514982	Hs.39991	efhand,S_100,S_100,efhand	S100 calcium-binding protein A2	4.0
	451282	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2,none	synaptotagmin 1	3.9
	433399	N48406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
30	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2,ubredoxin;TM=M;S	trichorhinophalangeal syndrome 1 gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
	453880	AI803166	Hs.135121	HSPT0,none	ESTs, Weakly similar to I38022 hypo	3.9
35	424125	M31689	Hs.1735	TGF-beta,TGFb_propeptide;	inhibit, beta B (activin AB beta po	3.9
	437377	AL39573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422652	AI562060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
	423220	AT745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly simila to AAB47496 NG	3.9
	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
40	411894	M57609	Hs.72916	zL-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
	425976	CT5094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87018	TM=Y;SS=M	hypothetical protein FLJ22938	3.8
	452679	Z42387	Hs.838883	tubulin-binding;TM=N;SS=M	transmembrane, prostate androgen in	3.8
45	421030	AW161357	Hs.101174	TM=M;SS=N	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92879	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HJH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calsynkin-2	3.8
	429440	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	428742	AA303828	Hs.181131	arf/ras,RecR,none	ESTs	3.8
	435818	AA700553	Hs.388614		ESTs	3.8
	420005	AW271106	Hs.133294		ESTs	3.8
55	410857	X63556	Hs.760	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402631	AB037745	Hs.104695	TM=M;SS=M	KIAA1324 protein	3.8
	449029	N28969	Hs.22891	aa_pombeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=M	MSTP031 protein	3.8
	443933	AI091531	Hs.203845	Ion_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
60	432952	AA813687	Hs.188173	histone,CBFD_NFYB_HMF;TM=	Homo sapiens cDNA FLJ12187 fis, clo	3.8
	424036	AA770688	Hs.348495	Pep_M12B_propep,Reproto	H2A histone family, member L	3.7
	453828	AW970960	Hs.293821	hormone_rec,zf-C4	ESTs	3.7
	407112	AA070801	Hs.51816		ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
	424651	AI493206	Hs.120785	trypsin;TM=M;SS=Y	ESTs	3.7
	409178	BE339498	Hs.50815	TM=N;SS=Y	kalikrein 5	3.7
	417059	AL037672	Hs.81671	Ca_channel_B,RepB_protein	extracellular matrix protein 1	3.7
	431194	D43704	Hs.250712	HCO3_cotransp;TM=Y;SS=N	calcium channel, voltage-dependent,	3.7
70	430397	AI924533	Hs.105807	SH3;TM=M;SS=N	bicarbonate transporter related pro	3.7
	416969	W33191	Hs.28907	MAGE;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	SAM_P3;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW368377	Hs.197568	ESTs, tumor protein 63 kDa with strong ho	3.7	
	418840	AI821614	Hs.185831		ESTs	3.7
	433573	AF234987	Hs.57652	7m_2,EGF,cadherin,amtini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.369382	thyroglobulin_1,IGFBP_2f-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neuronatin	3.7
	435114	AA775483	Hs.288936	ODC_AZ,Ribosomal_I9_N;TM=	mitochondrial ribosomal protein L9	3.7
	416899	BE262645	Hs.80420	II8;TM=M;SS=M	small inducible cytokine subfamily	3.7
	422110	AI376736	Hs.121555	kaesl,none	secreted protein, acidic, cysteine-	3.7
75	448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77667	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	AI2277829	Hs.111882	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

			RNase_HII;TM=N;SS=M	ribonuclease H1, large subunit	3.6
5	450663	H43540	Hs.25292	zf-C2H2;none	ESTs
	417387	AW021102	Hs.21509	PDZ_Guanylate_kin;TM=N;SS	tight junction protein 3 (zona occ)
	450825	AC035954	Hs.25527	ig;TM=Y;SS=M	B7 homolog 3
	439755	AW748482	Hs.77873		ESTs
	439873	BE159253	Hs.300638	kinase,none	ESTs
	439039	A1656707	Hs.48713	ank;TM=N;SS=N	neurotigin
	419235	AW470411	Hs.288433	EGF_fn1,vwc,vwd,MAM,Kerat	cyclin-dependent kinase inhibitor 2
	445033	AV652402	Hs.72901	Sema,TIG,PSI,GDI	Zonadhesin
10	404394	AF332975	Hs.307004	TM=M;SS=N	SEX gene
	452222	AW806287	Hs.21432		B-cell CLL/lymphoma 9
	422661	Y13620	Hs.122607		ESTs, Weakly similar to T32554 hypo
	420988	AW006352	Hs.159643	zf-C2H2,TFIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 kine
	439680	AW245741	Hs.58461	Ig,SET,PHD,zf-CXXC_Adap_c	ESTs, Weakly similar to K1CL_HUMAN
	426281	D59505	Hs.351344	fn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA
15	437446	AA789946	Hs.101302	eHand;TM=M;SS=N	calbindin 2, (29kD, calretinin)
	421690	AW162667	Hs.106857		Homo sapiens cDNA FLJ13558 fs, clo
	453939	AA418160	Hs.86043		v-erb-b2 avian erythroblastic leuka
	426158	NM_001982	Hs.199067	Furin-like,kinase,Recep_	membrane-associated tyrosine- and t
	439246	AI498072	Hs.351474	ank,kinase,UPF0073;TM=N;	85 kDa retinoblastoma protein bindl
20	410653	BE383768	Hs.65238	zf-C3HC4,AIP3;TM=M;SS=N	gb:RC1-HN0015-040400-011-d03 HN0015
	412703	AW984744			Homo sapiens, clone IMAGE:3507281,
	427871	AW992406	Hs.352406	TM=M;SS=N	fibronodulin
	444273	AI903474	Hs.230	LRR,LRRNT;TM=M;SS=M	ESTs
	434936	A1285970	Hs.183817	UCH-2	Homo sapiens, alpha-1 (VI) collagen
25	457889	AI077186	Hs.108885	vwa,Collagen;TM=M;SS=M	hypothetical protein FLJ20539
	422575	AK000546	Hs.118552	PTTR2;TM=Y;SS=M	ESTs
	428243	ALD43021	Hs.12705	WD40;TM=N;SS=M	sema domain, immunoglobulin domain
	426716	NM_006373	Hs.171921	Ig,Sema,PSI;TM=N;SS=M	flavin containing monooxygenase 2
	423778	Y05257	Hs.132821	FMO-like,pyr_reduct;TM=Y;S	ATP-binding cassette, sub-family A
30	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ESTs
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	- Homo sapiens cDNA FLJ11685 fs, clo
	447041	AI135486	Hs.250705		Homo sapiens cDNA FLJ12797 fs, clo
	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	tumor protein DS2-like 1
	446945	AI93115	Hs.16611	TM=M;SS=N	pyrrolidine-5-carboxylate reductase 1
35	416322	BE019494	Hs.79217	PSCR,NAD_Gly3P_dh,Octopin	ESTs, Moderately similar to KIAA121
	447347	AA570056	Hs.122730	NA;NA	hypothetical protein FLJ22318
	448984	AW751955	Hs.22753	TM=M;SS=N	actin related protein 23 complex,
	421778	AA428000	Hs.283072	NA;NA	homeo box C11
40	423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	uracil-DNA glycosylase 2
	432545	X52486	Hs.3041	cyclin,none	ESTs
	408495	WE8796	Hs.237731		major histocompatibility complex, c
	406851	AA609784	Hs.352392	Ig,MHC_II_beta;TM=M;SS=Y	Snf2-related CBP activator protein
	418736	T18979	Hs.87908	helicase,CAT_hook,SNF2_N	3-hydroxy-3-methylglutaryl-Coenzyme
45	410197	NM_005518	Hs.59889	HMG_CoA_synth;TM=N;SS=N	myo-inositol 1-phosphate synthase A
	453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	chondroitin sulfate proteoglycan 2
	417259	AW903B38	Hs.81800	EGF,g,lectin_c,sushi,Xii	ESTs
	453985	N44545	Hs.251865	Ph,none	heat shock 90kD protein 1, alpha
	412634	U85984	Hs.356531		ESTs, Weakly similar to ALU1_HUMAN
50	407204	R41933	Hs.140237	histone,histone	forkhead box M1
	444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	ESTs
	447334	AA515032	Hs.81108		complement component 4A
	426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,prey	sparc/osteonectin, cwcv and kazal-I
	419749	X73608	Hs.93029	kazal,thyroglobulin_1;TM=	ESTs
55	423595	R82826	Hs.220702	homeobox,none	major histocompatibility complex, c
	406673	M34996	Hs.198253	Ig,MHC_II_alpha;TM=M;SS=M	Homo sapiens mRNA, complete
	434241	AF118913		TM=N;SS=M	Homo sapiens cDNA: FLJ22528 fs, cl
	412490	AW803564	Hs.288850		KIAA1223 protein
	452277	AL049013	Hs.28783	ank;TM=M;SS=N	integrin, alpha 11
60	431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	HSPC037 protein
	421777	BE552088	Hs.108196	TM=M;SS=N	hypothetical protein FLJ20041
	453082	H18835	Hs.31608	Ion_trans;TM=Y;SS=M	aldehyde dehydrogenase 1 family, me
	414085	AA114016	Hs.75745	aldehd;TM=N;SS=M	Homo sapiens, Similar to RIKEN cDNA
	440300	N39760	Hs.8889	TM=M;SS=N	hypothetical protein FLJ2041
	400290	H18836	Hs.31608	Cys_knot	glioblastoma overexpressed
65	433339	AF019226	Hs.8036	ras,arf;TM=M;SS=N	lenomodulin protein
	419301	AA236166	Hs.132957	TM=Y;SS=M	hypothetical protein FLJ23309
	414792	BE314949	Hs.87128	TM=Y;SS=M	ESTs, Highly similar to T46395 hypo
	451428	AW803884	Hs.11057		Homo sapiens, clone IMAGE:3544662,
	432210	AI557421	Hs.273330	EGF,kazal,leminin_EGF,lam	glycosyltransferase
70	452242	R50958	Hs.159993		ESTs
	450878	AI147165	Hs.279727	TM=M;SS=N	partner of RAC1 (arafipin 2)
	413014	AW250533	Hs.75139	CTF_NFLnone	Homo sapiens mRNA; cDNA DKFZp584H19
	427919	AA173942	Hs.328416	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2
75	424005	AB033041	Hs.137507	RhoGAP;TM=M;SS=N	KIAA0712 gene product
	422072	AB018255	Hs.111138		ESTs
	440995	T57773	Hs.10263	homeobox;TM=N;SS=M	BerH-like homeobox 2
	428150	NM_003658	Hs.167218	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436
	416877	BE388286	Hs.85658	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase
80	452191	AU076408	Hs.28309	rnm,none	hypothetical protein FLJ20171
	450273	AW286454	Hs.24743	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr
	456177	NM_012391	Hs.79414	chromc;TM=N;SS=M	ESTs
	423062	NM_003655	Hs.5637	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1
	421848	X15880	Hs.108885		3.3

	433577	AW007080	Hs.284192		ESTs	3.3
	409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	CTF_NFI;none	Nuclear factor I/B	3.3
	422940	BE077458		Sec7,PH,ANF_receptor;Ig_	gb:RC1-BT0606-090500-01S-b04 BT0606	3.3
5	410001	AB041036	Hs.57771	Iyprsin;TM=M;SS=M	kellkrein 11	3.3
	427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein_MGC13010	3.3
	453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
	443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein_XPA-binding protein 2	3.3
	456034	AW450979			gb:Ui-H-B13-sla-a-12-0-Ui.1 NCL_CG	3.3
10	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
	412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
	426690	AW956329	Hs.23721	sugar_b;Ribosomal_S25	ESTs	3.3
	423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
15	437275	AW976035	Hs.292396	Frizzled;F2	ESTs, Weakly similar to AA7582_B-ca	3.3
	437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3438	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp566I133	3.3
	451691	AB089278	Hs.208162	C2	ESTs	3.3
	430433	AA478883	Hs.237766	WW;none	ESTs	3.3
	429343	AK000765	Hs.199480	VHS,ENTH,UTM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
	450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AI088490	Hs.249107		ESTs, Weakly similar to AA7582_B-ca	3.3
20	452679	AA131657	Hs.23830	CN_hydrolase	Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	409960	BE261944	Hs.355264		ESTs, Weakly similar to P4HA_HUMAN	3.3
	406850	AI624300	Hs.172928	wvc,Collagen,COL,Fk;TM=M;S	ESTs	3.3
	453674	AW591783	Hs.36131		ESTs	3.3
	425864	AW898928	Hs.9071	homeobox;none	ESTs	3.3
25	428412	AA428240	Hs.126083		hexokinase 1	3.3
	430316	NM_000875	Hs.239176	f13,Furin-like;pkinkase,Ra	collagen, type I, alpha 1	3.3
	440087	W28969	Hs.7718	KCNA,Ribosomal_S4e,S4,rm;	collagen, type XIV, alpha 1 (undul	3.2
	449933	AW157098	Hs.324104	DUF176;efhand;TM=M;SS=N	progesterone membrane binding prote	3.2
	441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs	3.2
30	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	insulin-like growth factor 1 recept	3.2
	422737	M26939	Hs.119571	Collagen,COLF;TM=N;SS=M	hypothetical protein FLJ22678	3.2
	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	424971	AA297005	Hs.154036	PH;TM=M;SS=N	ESTs, Weakly similar to T23273 hypo	3.2
	407669	AI827976	Hs.24391	efhand;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	collagen, type III, alpha 1 (Elters	3.2
35	426591	AK001155	Hs.214410		DKFZP586L151 protein	3.2
	414081	AW569976	Hs.365705	gl2;TM=N;SS=Y	tumor suppressing subtransferable c	3.2
	408795	AW749126	Hs.170345	hormone_rec;zf-C4	hypothetical protein FLJ13612	3.2
	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	7-dehydrocholesterol reductase	3.2
	437879	BE262082	Hs.5894	TM=N;SS=N	Homo sapiens cDNA FLJ10674 fis, clo	3.2
40	407872	AB039723	Hs.40735	Fz;Frizzled,7tm_2,DUF81;T	matrix Gla protein	3.2
	427289	AI097346	Hs.323878	aminotriat_5,SDF;none	hypothetical protein FLJ13710	3.2
	432375	BE536069	Hs.29562	efhand_S_100;TM=N;SS=M	hypothetical protein FLJ20515	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	hypothetical protein FLJ10305	3.2
	412774	A120865	Hs.380149	hormone_rec,zf-C4	frizzled (Drosophila) homolog 3	3.2
50	445842	T80334	Hs.13479	TM=M;SS=N	phosphoserine aminotransferase	3.2
	439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	S100 calcium-binding protein P	3.2
	414774	X02419	Hs.77274	kringle,hypen,plant_thl	procollagen C-endopeptidase enhance	3.2
	433336	AF017986	Hs.31386	Fz,NTR;TM=N;SS=M	ESTs	3.2
	439905	AW797755	Hs.110953	HLH;TM=M;SS=N	hypothetical protein FLJ20847	3.2
55	420251	AW374966	Hs.379829		hypothetical protein FLJ20980	3.2
	413004	T35901	Hs.75117	zf-C2H2;TM=N;SS=M	plasminogen activator, urokinase	3.2
	418688	Z266830	Hs.87268	annexin;TM=M;SS=N	secreted frizzled-related protein 2	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	retinoic acid induced 1	3.2
	424391	BE550112	Hs.158549		Human DNA sequence from clone RP5-1	3.2
60	440409	AW294316	Hs.125608	thored	interleukin enhancer binding factor	3.2
	452689	F33868	Hs.284176	transferin,KH-domain,rrm	annevin AB	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4,none	hypothetical protein FLJ14117	3.2
	434384	AA631910	Hs.370133		ESTs, Weakly similar to T203_HUMAN	3.2
65	413456	AF238083	Hs.68061	DAGK;TM=M;SS=N	ESTs	3.2
	431663	NM_015569	Hs.267182	T-box;TM=M;SS=N	transferin	3.2
	432874	W94322	Hs.279851	SH3;TM=M;SS=Y	nuclear receptor subfamily 1, group	3.2
	436252	AI539519	Hs.142827		ESTs	3.2
	421044	AF061871	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	sphingosine kinase 1	3.2
70	419102	AA234098	Hs.42424		TBX3-Iso protein	3.2
	419359	AI043202	Hs.90073	CAS_CSE1;TM=M;SS=N	melanoma inhibitory activity	3.2
	441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	Homo sapiens cDNA FLJ11562 fis, clo	3.2
	426418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	Human DNA sequence from clone RP1-2	3.2
	413076	U10564	Hs.75188	phosphatase;TM=M;SS=N	ESTs, Weakly similar to 2004399A.ch	3.2
	407874	A1766311	Hs.289047	COQ7	chromosome segregation 1 (yeast) hom	3.2
75	448019	AW947164	Hs.195641		interleukin-4 induced gene-1 protein	3.1
	427024	AA397572	Hs.348902		collagen, type IV, alpha 5 (Alport	3.1
	410281	AF076612	Hs.166185	vwc;W2,MA3,MIF4G	wee1 (S. pombe) homolog	3.1
	447205	BE817015	Hs.11006	LEA,paripin;TM=M;SS=N	Homo sapiens cDNA FLJ14059 fis, clo	3.1
	434433	AW629759			ESTs, Moderately similar to I38022	3.1
80	439737	A1751438	Hs.41271	C1q,Collagen,none	chromosome 11 open reading frame 14	3.1
	450157	AW981576	Hs.60178	PH,Band_41,RhoGEF,none	Homo sapiens clone 23928 mRNA sequ	3.1
	445989	H97754	Hs.11108		ESTs, Moderately similar to T17372	3.1
	442213	N36110	Hs.305971	sugar_b;TM=Y;SS=M	gb:hh70e05.y1 NCL_CGAP_GU1 Homo sap	3.1
					Homo sapiens mRNA full length Iner	3.1
					ESTs	3.1
					ESTs	3.1
					solute carrier family 2 (facilitate	3.1

	402496	Hs.6454	PDZ;TM=N;SS=M	Target_Exon	3.1
	438974	AF069816	Hs.62492	chromosome 19 open reading frame 3	3.1
	439335	AA742697	Hs.73798	NM_052863:Homo sapiens secretoglobin	3.1
5	412276	BE262621	MIF_sugar_tr,none	macrophage migration inhibitory fac	3.1
	416950	AL049798	Hs.80562	dermolopin	3.1
	456157	AW979153	Hs.336881	ESTs	3.1
	452753	AA028049	Hs.277729	SEC14 (S. cerevisiae)-like 2	3.1
	414420	AA043424	Hs.76095	immediate early response 3	3.1
10	446229	AI744964	Hs.14449	KIAA1609 protein	3.1
	453143	AA382234	Hs.356289	protein tyrosine phosphatase, recep	3.1
	411441	AL042355	Hs.70202	WD repeat domain 10	3.1
	422921	BE062045	Hs.351625	Homo sapiens cDNA: FLJ23260 fis, cl	3.1
	444441	AW613841	Hs.301394	hypothetical protein MGC3101	3.1
15	436729	BE621807	Hs.351316	transmembrane 4 superfamily member	3.1
	427890	AA435761	Hs.373623	ESTs	3.1
	444836	AV651680	Hs.208958	ESTs	3.1
	427876	AA494291	Hs.359171	ESTs	3.1
	413040	AA193338	Hs.12321	sodium calcium exchanger	3.1
20	427515	T79526	Hs.179516	Integral type I protein	3.1
	451092	AI207256	Hs.13768	Homo sapiens mRNA for FLJ00074 prot	3.1
	442222	AI061301	Hs.164773	ESTs	3.1
	452613	AA461599	Hs.23459	ESTs	3.1
	447191	NM_014621	Hs.17687	SH3-domain binding protein 4	3.1
	412690	T85247	Hs.351875	cytochrome c oxidase subunit Vtc	3.1
25	418313	BE244231	Hs.84038	CGL-08 protein	3.1
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APA	3.1
	434042	AI589941	Hs.8254	Homo sapiens, Similar to tumor diff	3.1
	420576	AA297634	Hs.54925	KIAA1858 protein	3.1
30	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (3.1
	424927	AW973665	Hs.153850	hypothetical protein C321D2.4	3.1
	440100	BE382885	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN	3.1
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.1
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (Eco	3.1
35	418444	AI902899	Hs.85155	butyrate response factor 1 (EGF-res	3.1
	423464	NM_016240	Hs.128866	CSR1 protein	3.1
	424804	AW865388	Hs.151076	KIAA1243 protein	3.1
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.1
	453271	AA903424	Hs.6786	ESTs	3.1
40	411274	NM_002776	Hs.69423	kalikrein 10	3.1
	434095	AA011117	Hs.3745	milk fat globule-EGF factor 8 proto	3.1
	403439			NM_031419:Homo sapiens molecule po	3.1
	413244	AW955951	Hs.159285	kruppel-related zinc finger protein	3.1
	411756	BE294350	Hs.71691	discoidin domain receptor family, m	3.1
	409007	AI122107	Hs.4959	Homo sapiens mRNA; cDNA DKFZp434G08	3.1
45	452547	AA335295	Hs.74120	adipose specific 2	3.1
	414359	ME2194	Hs.75829	cadherin 11, type 2, OB-cadherin (o	3.1
	432121	BE218049	Hs.121820	ESTs	3.1
	449123	D50920	Hs.23106	KIAA0130 gene product	3.1
50	431176	AI026984	Hs.293662	ESTs	3.0
	419245	AI732742	Hs.87440	ESTs	3.0
	434493	AA635305	Hs.376591	hypothetical protein FLJ14299	3.0
	449177	BE516694	Hs.288042	RNB6	3.0
	430449	AA352723	Hs.241471	hypothetical protein DKFZp761F241	3.0
55	452887	AI702223	Hs.107253	DKFZP564D0764 protein	3.0
	451678	AA374181	Hs.26799	camillina O-octanoyltransferase	3.0
	445457	AF168793	Hs.12743	Homo sapiens brother of COO (SOC) m	3.0
	407697	AA043925	Hs.339352	Interferon, alpha-inducible protein	3.0
	431629	AI077026	Hs.265827	KIAA1442 protein	3.0
60	432302	AA345857	Hs.274307	TNF receptor-associated factor 4	3.0
	442549	AI751601	Hs.8375	KIAA1856 protein	3.0
	437959	AI472068	Hs.375604	hypothetical protein FLJ20316	3.0
	447400	AK000322	Hs.18457	Homo sapiens DNA from chromosome 19	3.0
	411734	AW374954	Hs.71779	hypothetical protein FLJ12656	3.0
65	443547	AI271273	Hs.356487	ESTs, Weakly similar to AIU7_HUMAN	3.0
	417000	BE277919	Hs.306019	KIAA0202 protein	3.0
	416987	D86957	Hs.80712	phosphatidylinositol-4-phosphate 5-	3.0
	424494	U78576	Hs.149255	ESTs	3.0
	414496	W73853	Hs.355424	hypothetical protein FLJ22637	3.0
70	413336	AI569936	Hs.296178	RAB26, member RAS oncogene family	3.0
	434314	BE392921	Hs.3797	C11000425:g 4507721 refNP_003310.	3.0
	401098			transmembrane, prostate androgen in	3.0
	418245	AA088757	Hs.83883	Human D9 splice variant B mRNA, com	3.0
	407688	W25317	Hs.37616	Cas-Br-M (murine) ectropic retrov	3.0
75	456906	AI17646	Hs.156637	M-phase phosphoprotein 6	3.0
	424744	AIW75781	Hs.152720	ESTs	3.0
	452195	AA894712	Hs.116878	bleomycin hydrolase	3.0
	415988	BE407713	Hs.78943	hypothetical protein FLJ12442	3.0
	418399	AF131781	Hs.84753	proteocadherin alpha 10	3.0
	420560	F09247	Hs.247735	C9000308:g 12737280 refXP_006682	3.0
80	404861			thrombospondin 4	3.0
	414152	NM_003248	Hs.75774	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
	421307	BE539976	Hs.103305	hypothetical protein	3.0
	444868	BE560471	Hs.12101		

450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
452864	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
422105	AI929700	Hs.111680	TM=M;SS=N	endosulfine alpha	3.0
422278	AF072873	Hs.114218	Fz;Fz2;7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
5	430677	Hs.124023		Homo sapiens cDNA FLJ14218 fs, cDNA	3.0
	412678	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD	3.0
	426801	AA486846	Hs.271795	ESTs, weakly similar to 138022 hypo	3.0
	421983	AI252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin)	3.0
10	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.0
	408812	ABD11084	Hs.48924	KIAA0512 gene product; ALEX2	3.0
	438746	AI085815	Hs.184727	Human melanoma-associated antigen p	3.0

TABLE 4B

15	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
20	Pkey	CAT Number	Accession
	418344	245371_1	AA218387 T63548 AA228676
	412703	1243670_1	AW984759 AW984744
	434241	63414_1	AF119913 AI207698 R57074
25	422940	58443_1	BC012771 BG397153 BF386195 AA337277 AA319285 AW843252
	456034	686586_1	AA136653 AA136655 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	434433	111338_1	AA633408 AW749955 AW629759 AJ651005

TABLE 4C

30	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
35	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	406387	9256180	Plus	116229-116371,117512-117651
	400496	8743564	Plus	41515-41695
	402496	9797769	Minus	8615-9103
40	403439	9719679	Plus	91463-91632
	401038	7232177	Minus	4277-4469
	404661	9797073	Plus	33374-33675,33769-34008

TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

50	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar accession number, GenBank accession number				
	UniGeneID:	UniGene number				
	Pred.Prot.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).				
	UniGene Title:					
55	R1:	Ratio of 90th percentile tumor to 50th percentile of normal body tissue				
	Pkey	ExAccn	UniGeneID	Pred.Prot.Domains	UniGeneTitle	R1
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
60	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXYD domain-containing ion transporter	13.7
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurturin growth-promoting f	13.7
	414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
	438091	AW373062	Hs.351548	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
	413815	AL046341	Hs.75562	pkinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	13.2
	439180	AI393742	Hs.199067	Fuin-like_pkinase_Recep_	v-erb-b2 avian erythroblastic leuke	13.2
	431441	U61961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.6
	452547	AA336295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
	452239	AW379378	Hs.356288		protein tyrosine phosphatase, recip	12.1
	441384	AA447843	Hs.288660	7tm_3,none	retinoic acid induced 3	11.9
70	419223	X60111	Hs.1244	transmembrane4(TM=Y;SS=M	CD9 antigen (p24)	11.7
	413859	AW982356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	11.5
	410667	U24389	Hs.65436	Lysyl_oxidase(TM=N;SS=M	lysyl oxidase-like 1	11.2
	422699	BE410590	Hs.119257	SH3_HST_Rep;TM=M;SS=N	ems1 sequenca (mammary tumor and sq	10.1
	419452	U33635	Hs.90572	Ig_pkinese(TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
	427378	BE516037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
	444784	D12485	Hs.11951	Somatomedin_B_Endonucleas	ectonucleofida pyrophosphatase/phos	9.9
	436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
	412926	AJ879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-rich	9.5
	426280	U31519	Hs.1872	PEPC_K(TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
80	432638	AA340864	Hs.278562	PMP22_Claudin(TM=Y;SS=M	claudin 7	9.4
	423778	Y09267	Hs.132821	FMO-like_py_redox(TM=Y;S	flavin containing monooxygenase 2	9.4
	424206	NM_003734	Hs.198241	Cu_enzyme_oxid,Cu_enzyme_ox	amine oxidase, copper containing 3	9.4
	444797	AB016333	Hs.12002	SH3_SAM(TM=M;SS=N	KIAA0790 protein	9.0

				PPAP2B Phosphatidic acid phosphatase type 2B	9.0	
				tensin	8.9	
				immunoglobulin superfamily containi	8.8	
				dealed In oral cancer (mouse, homo	8.7	
				hypothetical protein	8.7	
5	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	RAB25 RAB25, member RAS oncogene fa	8.6
	443932	AW886222	Hs.8973	SH2;WW,PID,none	SH3-domain protein 5 (ponsin)	8.6
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	folisatin-like 1	8.5
	433892	NM_004642	Hs.3436	TM=M;SS=N	hypothetical protein FLJ20041	8.5
	410568	BE379794	Hs.158651	death TNFR_c6;TM=Y;SS=M	nuclear receptor subfamily 1, group	8.4
	433662	W07162	Hs.150826	ras,ABC_intron,arf;TM=M;SS=	v-abl-b2 avian erythroblastic leuke	8.3
	421853	AL117472	Hs.106924	SH3,Sorb;TM=M;SS=N	SH3-domain binding protein 4	8.2
	425335	BE394327	Hs.296267	efhand,kaeal,arf,ras,7tm_	amino acid transporter system A1	8.2
10	400290	H18836	Hs.31608	Cys_knot	G protein-coupled receptor 56	8.1
	438089	W05391	Hs.351546	hormone_rec,zf-C4,none	solute carrier family 2 (facilitate	8.1
	426158	NM_001982	Hs.199067	Furin-like,phluas8,Recep_	integrin, alpha 7	8.1
	447191	NM_014521	Hs.17657	SH3;TM=M;SS=N	myosin VI	8.1
	439941	AJ392640	Hs.18272	Aa_trans;TM=Y;SS=N	transmembrane 4 superfamily member	8.0
15	439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	glycerol-3-phosphate dehydrogenase	7.9
	442213	N38110	Hs.305371	sugar_tr;TM=Y;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	412649	NM_002205	Hs.74369	integrin_A,FG-GAP;TM=M;SS	wee1 (S. pombe) homolog	7.9
	448913	AA194222	Hs.22554	rrm,zt-RanBP,phosphatase,GST_	myosin regulatory light chain 2, sm.	7.7
	420168	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	junction plakophilin	7.6
20	407102	AA007629	Hs.348601	TM-N;SS=M	DKFZP586G1122 protein	7.6
	452516	AA058630	Hs.29759	phkase;TM=M;SS=N	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
	443076	U010564	Hs.75188	efhand;TM=M;SS=N	H.sapiens mRNA for 3'UTR of unknown	7.5
	443604	C03577	Hs.9815	Armadillo_seq;TM=M;SS=N	plakophilin 3	7.4
	429002	AW248439	Hs.2340	Armadillo_seq;TM=M;SS=N	famlin, light polypeptide	7.4
25	432562	BE631048	Hs.278422	zf-C2H2;TM=M;SS=N	hexokinase 1	7.3
	426359	A3378409	Hs.10882	adenylatekinase,none	ephrin-A1	7.3
	417733	AL048678	Hs.82503	NA;NA	von Willebrand factor (VWF), mRNA	7.1
	451541	BE279383	Hs.26557	Armadillo_seq;TM=M;SS=N	chromosome 19 open reading frame 3	7.1
	443951	F13272	Hs.358835	P2M/P22_Claudin,none	retinoid acid receptor responder (L	7.0
30	409960	BE261944	Hs.355264		cargo selection protein (mannose 6	7.0
	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,ww,wwc	small nuclear ribonucleoprotein pol	7.0
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	hypothetical protein FLJ22415	6.9
	417771	AAB04698	Hs.82547		p75NTR-associated cell death execut	6.9
35	424118	BE269041	Hs.140452	parilipin;TM=N;SS=M	frizzled (Drosophila) homolog 6	6.9
	402705	X76951	Hs.180909	AtpC-TSA;TM=M;SS=M	protein phosphatase 1, regulatory (6.9
	417115	AW952792	Hs.334612	Srn,phkase;TM=N;SS=N	Homo sapiens, clone MGC:9381, mRNA,	6.9
	442572	AI001922	Hs.136121	HSP70	transmembrane 4 superfamily member	6.9
	447216	R76812	Hs.169248	cytochrome_c;NA;NA	hypothetical protein	6.9
40	422278	AF072673	Hs.114218	Fz,Frtzled,7tm_2;TM=Y;SS	ESTs, Moderately similar to A58194	6.8
	414857	A4424074	Hs.76780		platelet-derived growth factor rece	6.7
	447528	A1612027	Hs.76277	TB2_DP1_L1VA22;TM=Y;SS=M	phosphoinositide-3-kinase, regulato	6.7
	436729	BE621807	Hs.351316	TM=Y;SS=M	UDP-N-acetylglucosamine pyrophospho	6.6
	428013	AF151020	Hs.181444	TM=Y;SS=M	fibroblast growth factor receptor 1	6.6
	444143	AW747996	Hs.160999	Bcl-2,none	CDC28 protein kinase 1	6.6
45	414443	AU077268	Hs.76144	tg,phkase;TM=Y;SS=N	laminin, beta 1	6.6
	418751	BE389014	Hs.372548	SH2,none	serum/glucocorticoid regulated kina	6.6
	448479	H96115	Hs.21293	UDPGT;TM=M;SS=N	Homo sapiens cDNA FLJ14201 fis, clo	6.5
	410652	X66946	Hs.748	tg,phkase,SH2,SH3,C2,PH,	Integrin, beta 5	6.5
	414883	AAB26960	Hs.348689	C3H;TM=N;SS=N	fibroblast growth factor receptor 3	6.5
50	417426	NM_002291	Hs.82124	laminin_EGF,laminin_Nterm	phosphoprotein enriched in astrocyt	6.5
	428179	AII27727	Hs.279696	pkinese,PX,phkase_C;TM=N	signal transduction protein (SH3 co	6.5
	443195	BE148235	Hs.193063	Aq_trans,none	protein tyrosine phosphatase, recep	6.5
	424512	X53002	Hs.149846	Integrin_B,EGF;TM=Y;SS=M	KIAA0512 gene product; ALEX2	6.4
55	421733	AL118671	Hs.1420	tg,phkase;TM=Y;SS=M	poliovirus receptor-related 2 (herp	6.4
	428950	BE311879	Hs.194573	DED;TM=M;SS=N	solute carrier family 7 (cationic a	6.4
	450172	NM_008864	Hs.24587	SH3,homone;TM=M;SS=N	immunoglobulin lambda locus	6.4
	416078	AL034349	Hs.79005		Interferon_alpha-inducible protein	6.4
	408912	A8011084	Hs.48024	Armedillo_seq;TM=M;SS=M	golgi phosphoprotein 2	6.4
60	426373	AT751658	Hs.163986	tg;TM=Y;SS=M	non-metastatic cells 4, protein exp	6.4
	449029	N28893	Hs.22891	aa_permeases;TM=Y;SS=M	KIAA1295 protein	6.4
	406621	X76809	Hs.161125	tg,HSP70,Ppx-GppA;TM=M;SS	NG22 protein	6.4
	431629	AU077025	Hs.265827	TM=M;SS=Y	discs, large (Drosophila) homolog 5	6.3
	428169	AI92984	Hs.182793	photRC,UPP0418;TM=Y;SS=N	v-ki6 Hardy-Zuckerman 4 feline sarc	6.3
65	443337	Y07604	Hs.9235	NDK;TM=N;SS=N	hypothetical protein FLJ22357 simil	6.3
	451282	A8037716	Hs.26204	SH3;TM=M;SS=N	CD209 antigen	6.3
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	vav 3 oncogene	6.3
	426539	AB011155	Hs.170230	SH3,PDZ,Guanylate_kin;TM=	cyclin-dependent kinase inhibitor 2	6.3
	417208	S67773	Hs.81655	tg,phkase;TM=Y;SS=M	cd2din domain receptor family, m.	6.3
70	438278	AE049248	Hs.57988	tpfRC,UPP0418;TM=Y;SS=N	ESTs	6.3
	429455	A472111	Hs.278694	ledin_c	collagen, type XV, alpha 1	6.2
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
	445033	AV652402	Hs.72901	amf;TM=N;SS=N	KIAA0251 protein	6.2
	411758	BE294350	Hs.71891	pkinese,F5_F8_type_C;TM=Y	potassium large conductance calcium	6.2
	453902	BE502341	Hs.3402		doublecortin and CaM kinase-like 1	6.2
75	416105	A168220	Hs.83164	Collagen,TSFN;TM=M;SS=M	progesterone membrane binding prote	6.2
	449924	W30681	Hs.146233	SH3,none	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
	426520	BE545984	Hs.343566	aa_permeases,pyridoxal_de	laminin, alpha 5	6.2
	453064	R40334	Hs.89463		tyrosine 3-monooxygenase/tryptophan	6.2
	448520	A8002367	Hs.21355	pkinese,DCX;TM=M;SS=N		
80	452683	AJ089575	Hs.374574	homeobox,none		
	402576	AF043329	Hs.173717	PAP2;TM=Y;SS=M		
	444672	Z95636	Hs.11659	laminin_EGF,laminin_G,EGF		
	450440	AB024334	Hs.25001	14-3-S;TM=M;SS=N		

				ESTs	6.1
				major histocompatibility complex, c	6.1
				ESTs	6.1
				Lutigeran blood group (Auberger b an	6.1
				Integrin, alpha 2 (CD49b, alpha 2 s	6.1
				hypothetical protein PP1057	6.1
				ESTs	6.0
				ESTs	6.0
				Homo sapiens cDNA: FLJ23165 fts, cl	6.0
				hypothetical protein FLJ12538 simil	5.9
				KDEL (Lys-Asp-Glu-Lys) endoplasmic	5.9
				geranylgeranyl diphosphate synthase	5.9
				macrophage migration inhibitory fac	5.9
				ubiquitin activating enzyme E1-like	5.9
				tyrosine 3-monooxygenase/tryptophan	5.9
				sterile-alpha motif and leucine zip	5.9
				cadherin, EGF LAG seven-pass G-type	5.9
				proliferation-associated 2G4, 38kD	5.9
				stress-induced-phosphoprotein 1 (Hs	5.9
				zinc/ferr regulated transporter-like	5.9
				type I transmembrane protein Fn14	5.8
				parvin, alpha	5.8
				low density lipoprotein receptor (f	5.8
				light junction protein 3 (zona occi	5.8
				phospholipase C, beta 3, neighbor p	5.7
				ATP-binding cassette, sub-family A	5.7
				uncharacterized hypothalamus protei	5.7
				nuclear receptor co-repressor 1	5.7
				C3002124:gi 12737280 ref XP_0086682	5.7
				protein tyrosine phosphatase, recep	5.7
				ESTs	5.7
				hypothetical protein FLJ10697	5.6
				platelet-derived growth factor rece	5.6
				phosphatidic acid phosphatase type	5.6
				ESTs, Weakly similar to 138022 hypo	5.6
				nuclear receptor co-repressor/HDAC3	5.6
				receptor (calcitonin) activity modi	5.6
				phospholipase A2, group IIa (plate	5.6
				calcium/calmodulin-dependent prot	5.6
				G protein coupled receptor interact	5.6
				nuclear receptor interacting protei	5.5
				development and differentiation enh	5.5
				ESTs, Weakly similar to ALU2_HUMAN	5.5
				H2A histone family, member X	5.5
				ESTs, Highly similar to G01887 MEK	5.5
				endosulfine alpha	5.5
				ESTs	5.5
				ephrin-A4	5.5
				receptor (calcitonin) activity modi	5.5
				Junctional adhesion molecule 1	5.5
				butyrate-induced transcript 1	5.5
				myosin, light polypeptide kinase	5.5
				mitogen-activated protein kinase 6	5.5
				protein tyrosine phosphatase, recep	5.4
				ATPase, Ca transporting, plasma mem	5.4
				pyrrolidine-5-carboxylate synthetase	5.4
				EphB3	5.4
				A kinase (PRKA) anchor protein 2	5.4
				HMT1 (hnRNP methyltransferase, S. c	5.4
				enigma (UM domain protein)	5.4
				ESTs	5.4
				heat shock 27kD protein family, mem	5.4
				ESTs, Moderately similar to 154374	5.4
				TNF receptor-associated factor 4	5.4
				Homo sapiens clone 24747 mRNA seque	5.4
				hypothetical protein FLJ20041	5.4
				peroxonase 2	5.4
				vascular endothelial growth factor	5.4
				solute carrier family 29 (nucleosid	5.4
				specifin, alpha, non-erythrocytic 1	5.3
				tetraspan NET-6 protein	5.3
				plasminogen activator, urokinase	5.3
				uridine monophosphate kinase	5.3
				ephrin-A3	5.3
				adrenergic, alpha-2A, receptor	5.3
				N-Acetylglucosamine kinase	5.3
				dual specificity phosphatase 5	5.3
				ESTs	5.3
				ESTs, Highly similar to JC5818 gamm	5.3
				thyroid hormone receptor interactor 6	5.3
				IMP (inosine monophosphate) dehydro	5.2
				cell division cycle 2-like 1 (PITSL	5.2
				transforming growth factor, beta re	5.2

407744	AB020529	Hs.38095	ABC_intron,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2	
448108	ALD36596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2	
422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2	
417098	AB017365	Hs.173859	Frizzled,Fz_7tm_2,toxin_2	frizzled (Drosophila) homolog 7	5.2	
5	430526	AF181862	Hs.242407	G protein-coupled receptor, family	5.2	
414176	BE140538	Hs.75794	7tm_3;TM=Y;SS=M	EDG-2 (endothelial differentiation	5.2	
416710	AI268325	Hs.54890	Peptidase_M9_EGF_Ig_Neur	hypothetical protein FLJ23590	5.2	
417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2	
10	413244	AW955951	Hs.159265	kruppel-related zinc finger protein	5.2	
421837	AF135163	Hs.108802	BTB_Pep_M12B_propep_Repro	N-ethylmaleimide-sensitive factor	5.2	
429379	NM_014840	Hs.200598	kinase_RIO1;TM=M;SS=N	KIAA0637 gene product	5.2	
429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2	
437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 8-ce	5.1	
421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHU1E coll	5.1	
15	440851	NM_002709	Hs.21537	protein phosphatase 1, catalytic su	5.1	
452568	AA805634	Hs.300870	PI3_PI4_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1	
452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1	
437175	AW968078	Hs.87773	pklnase_pklnase_C,none	protein kinase, cAMP-dependent, cat	5.1	
437056	AI147061		specifin,SH3,PH,CR	gbook33at1,s1 Scores_NSF_F8_9W_OT_P	5.1	
20	450998	BE387614	Hs.25797	splice factor 3b, subunit 4, 49kD	5.1	
444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGCG3101	5.1	
448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1	
452345	AA293278	Hs.29173	DSPC;TM=M;SS=N	hypothetical protein FLJ20515	5.1	
25	443412	WB4893	Hs.9305	angiotensin receptor-like 1	5.1	
412853	M34175	Hs.74626	Adaptin_N_AltapinC2	adaptor-related protein complex 2,	5.1	
439866	AA280717	Hs.5727	rrm;NTF2;TM=M;SS=N	Res-GTPase activating protein SH3 d	5.1	
439975	AW968081	Hs.6817	Harm1p_Iike;TM=M;SS=N	Inosine triphosphatase (nucleoside	5.1	
436523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1	
30	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	5.1	
412641	M16660	Hs.74335	HSP70_1g_Ppx-GppA;TM=M;SS	heat shock 90kD protein 1, beta	5.1	
431236	AV656840	Hs.285115	fr3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1	
436552	AJ245820	Hs.6314		type I transmembrane receptor (selz	5.0	
422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0	
35	427502	AI811855	Hs.7133	Homo sapiens, clone IMAGE:3161564,	5.0	
414166	AW888941	Hs.75789	DEAD_helicase_C,nm,Ndr,C	N-myc downstream regulated	5.0	
424954	NM_000546	Hs.1846	P53_WD40_IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0	
422059	AA523172	Hs.103135	REJ_PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFRA_HUMAN	5.0	
426836	BE242634	Hs.2055	TMF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0	
40	410793	AW581906	Hs.66392	SH3_afhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 6B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

437056 428504_3 AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

60 Pkey Ref Strand Nt_position
 405484 5922025 Plus 199214-199579,199672-199920,200262-20049

65 TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

70 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI681793	Hs.285529	G protein-coupled receptor 49	24.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
10	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.50
	444783	AK001468	Hs.62180	anillin (<i>Drosophila</i> Scraps homolog), act	21.15
	415989	AI267700	Hs.317584	ESTs	20.95
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metap	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
15	421470	R27498	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
	450531	AW301032	Hs.203800	ESTs	16.80
	432667	AW016936	Hs.233364	ESTs	16.35
	443211	AI128388	Hs.143655	ESTs	15.80
20	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	406964	M21305	Hs.125395	gb:Human alpha satellite and satellite 3	15.00
	410355	SS8544	Hs.153057	spenn associated antigen 1	14.70
	441377	BE218239	Hs.202656	ESTs	14.45
	413318	AU076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MSC1543B	14.35
25	440304	BE159984	Hs.125395	ESTs	14.25
	428427	M88699	Hs.169840	TTK protein kinase	13.60
	451561	NS2812	Hs.177403	ESTs	12.80
	434032	AW009951	Hs.206892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	12.55
30	428684	AK001666	Hs.189095	similar to SALL1 (sal (<i>Drosophila</i>)-like	12.40
	446232	AI281848	Hs.194691	retinol acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132853	Zic family member 2 (odd-paired <i>Drosophi</i>	11.85
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
35	452461	N78223	Hs.106106	transcription factor	11.42
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400634				11.00
	448706	AW291095	Hs.21814	Interleukin 20 receptor, alpha	10.75
	453668	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
	426890	AA393167	Hs.41294	ESTs	10.60
40	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.60
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp584F093 (fr	10.40
	425761	AW664214	Hs.196729	ESTs	10.25
	404567				10.15
45	428536	AI143139	Hs.2288	vslm1-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
	459504	BE514127		gb:601316974F1 NIH_MGC_8 Homo sapiens cD	9.95
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE378594	Hs.49136	ESTs, Moderately similar to ALU1_HUMAN A	9.85
50	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
	420900	AL045633	Hs.44269	ESTs	9.68
	438639	AI278360	Hs.31409	ESTs	9.55
	439521	AI1808955	Hs.58248	ESTs	9.55
	445576	AI247763	Hs.16928	ESTs	9.50
55	408489	AI082437	Hs.26580	ESTs	9.50
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.98
	400195	NA		NA	8.90
	411785	H43346		gbyp09a04.r1 Soares breast 3NbHBst Homo	8.90
60	418895	AA894638	Hs.14800	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (<i>S. cerevisiae</i>)-like, magnesium hor	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
	414559	AV856184	Hs.76452	C-reactive protein, pentraxin-related	8.64
	445436	A1224105	Hs.151408	ESTs	8.50
65	403776				8.50
	433447	U20195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
	422505	AL120862	Hs.124166	ESTs	8.25
	453242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
70	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	A1563695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8493	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443450	N66045	Hs.133529	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
10	400250	NA		NA	7.53
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404956				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
15	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23820	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
20	416143	AIS55650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	455553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	7.15
25	421373	AA806229	Hs.167771	ESTs	7.10
	418763	AK000219	Hs.89367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
30	413573	A1733859	Hs.149089	ESTs	6.95
	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CG-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
35	422711	D60541	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586L1518 (f	6.82
	457030	A1301740	Hs.173381	dihydroxyacetonephosphate-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31684	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1-to S and G2 to	6.69
45	405747	A1925153	Hs.217493	annexin A2	6.65
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2255	secretory granule, neuroendocrine protein	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	A4889120	Hs.110537	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	6.50
	418454	A4315308	Hs.1955870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	weak autoantigen with coiled coil domain	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	A1A21086	Hs.10592	ESTs	6.47
	406871	AA129547	Hs.285764	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452839	U65011	Hs.30743	preferentially expressed antigen in melan	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	A8011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AN05457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	A356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032859	Hs.318584	novel C3HC4 type Zinc finger (ring finger	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-es	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	Moderately similar to reduced expr	6.30
	409918	BE313525	Hs.57435	acute carrier family 11 (proton-coupled	6.25
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	416857	AA188776	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.16
	420096	AA775910	Hs.95011	synaptophysin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.223320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.11
	424746	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172406	cell division cycle 27	6.08
	407771	AL138272	Hs.52713	ESTs	6.08

	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
5	412246	A1160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418568	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	416421	AA134008	Hs.79306	eukaryotic translation initiation factor	5.95
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fts, clone NT	5.90
	409913	BE243642	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE286227	Hs.250822	serine/threonine kinase 15	5.86
15	413585	A1133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA FLJ10518 fts, clone NT	5.85
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ11041 fts, clone NT	5.85
	441645	A122279	Hs.201655	ESTs, Weakly similar to T23405 hypothetical	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
20	408687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fts, clone PL	5.82
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040620	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58967	glycan 4	5.78
	423806	AA331247	Hs.66617	ESTs	5.77
25	454036	AA374756	Hs.93550	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000262	Hs.239681	hypothetical protein FLJ20276	5.75
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical	5.75
	442957	A1949952	Hs.49397	ESTs	5.75
30	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134328	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystein SN	5.69
35	433687	AA743991	Hs.102651	gb\m57p01.s1 NCL_CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482	Hs.90012	gb\HA2093 Human fetal liver cDNA library	5.68
	452608	M45202	Hs.301957	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
40	451177	A1959716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
	436217	T53925	Hs.107	#fringen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.55
45	426235	AI631984	Hs.34447	ESTs	5.55
	445640	AW965626	Hs.31704	ESTs, Weakly similar to KIAA0227 [Hsap]	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	5.52
	442980	AA857025	Hs.8878	kinase-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
55	441421	AA356702	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.19445	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AM23056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	416139	AW975942	Hs.48524	ESTs	5.30
65	412140	AA219691	Hs.73625	RABG interacting, kinesin-like (rebbikines	5.29
	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
70	436016	AA806455	Hs.121538	Human DNA sequence from clone RP1-472E5	5.25
	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453821	AI824009	Hs.44577	ESTs	5.25
	413582	AW205847	Hs.71331	hypothetical protein MGCS360	5.25
	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypothetical	5.25
75	407884	BE075316	Hs.95011	synapsin, beta 1 (dystrophin-associated	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110825	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16988	hypothetical protein FLJ11046	5.20
	441795	N5B115	Hs.21137	AD024 protein	5.20
80	449416	A1651016	Hs.246311	ESTs	5.20
	418379	AA216940	Hs.137516	fidgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 [40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site family	5.15
	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical protein	5.15
5	447713	AI420733	Hs.207083	ESTs	5.15
	425739	T19016	Hs.159410	molybdoenzyme synthase sulfurylase	5.15
	420170	UA3374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
	441139	AW449009	Hs.126647	ESTs	5.13
10	451121	AW973795	Hs.126927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI971313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
	422805	AAA36898	Hs.121017	H2A histone family, member A	5.07
15	411750	SE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
20	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.06
	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA		NA	5.00
25	408562	AM36323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	I95348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430789	AA632577	Hs.310235	ESTs, Weakly similar to J78885 serine/th	4.90
30	425420	BE535911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379846	Hs.6904	Homo sapiens mRNA full length Insert cDNA	4.90
	418612	AB037788	Hs.224061	cleavage and polyadenylation specific fa	4.90
	439927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
35	450588	AL050708	Hs.25159	Homo sapiens cDNA FLJ10794 fis, clone NT	4.88
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN 8	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.87
	421128	M74587	Hs.102122	insulin-like growth factor binding prota	4.86
	411835	U28843	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
40	418396	AT765805	Hs.26691	ESTs	4.85
	430510	AN162916	Hs.241576	hypothetical protein PRG2577	4.84
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW448612	Hs.152475	ESTs	4.71
45	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA		NA	4.70
	451807	WS2854	Hs.27099	hypothetical protein FLJ23283 similar to	4.68
	436862	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14881	4.68
	410044	BE556742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
50	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410558	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
55	422892	AA988176	Hs.121563	hypothetical protein FLJ20641	4.65
	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA182669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
	412723	AA640459	Hs.395951	hypothetical protein AF301222	4.59
60	425745	U44060	Hs.14427	Homo sapiens cDNA FLJ21800 fis, clone H	4.59
	452795	AN392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429582	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
65	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121688	ESTs, Moderately similar to PC4259 ferni	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	418467	H57585	Hs.37467	ESTs	4.55
70	408867	AA437199	Hs.656	cell division cycle 25C	4.54
	419423	D26488	Hs.90316	KIAA0007 protein	4.54
	414132	AI801235	Hs.46480	ESTs	4.53
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acetyl	4.50
	451009	AA013140	Hs.115707	ESTs	4.50
75	431064	AI903735	Hs.656	gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AI137496	Hs.9001	ESTs	4.50
	400288	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
	410486	AW235094	Hs.69233	zinc finger protein	4.50
	428632	AF157326	Hs.184786	TBP-interacting protein	4.50
80	429762	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408380	AI123050	Hs.44532	ubiquitin	4.49
	423936	U77629	Hs.135639	actin-acid-sucrose complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S6	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE187434	Hs.98471	ESTs, Weakly similar to T18712 hypothes	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
5	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA	NA	NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
10	412359	AW837985	gb:QV3-LT0048-140200-083-e05	LT0048 Homo	4.40
	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	HS9846	Hs.126355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419780	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284968	Hs.266308	mosaic serine protease	4.40
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	AT99376	gb:BT34507.x1	NCI_CGAP_Ov23 Homo sapiens	4.37
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
20	459574	AT741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
	448243	AW369771	He.52620	integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.36
	448152	A1292036	Hs.150288	ESTs	4.34
	435580	AF086401	Hs.239347	ESTs, Moderately similar to S65657 alpha	4.32
25	438211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.28352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	438619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothes	4.30
30	458076	R80081	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subunit	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW865757	Hs.257862	ESTs	4.25
	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL136352	Hs.265683	ESTs, Weakly similar to I38022 hypothes	4.25
	409298	AL137163	Hs.57549	hypothetical protein dJ473B4	4.24
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
40	424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like	4.20
	446912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005686	Hs.134779	EST	4.20
45	411893	R82845	Hs.237389	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163	gb:con52g03.y5	NCI_CGAP_Co8 Homo sapiens	4.20
	404516	NA	NA	NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AB227237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcoplasmic-associated protein	4.16
55	433159	AB035898	Hs.150587	kinesin-like protein 2	4.16
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFzp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-84 protein	4.15
	428692	A372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA161520	Hs.334822	hypothetical protein MGC4486	4.15
	414538	AW161222B	Hs.107987	ESTs	4.14
	453931	AI121278	Hs.25144	ESTs	4.12
	427718	A798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	transducin-like calcium-binding protein	4.10
65	440209	H05040	Hs.22269	neurexin 3	4.10
	435148	A918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167631	methylcrotonyl-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothes	4.10
70	441488	A133165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rrp40	4.10
	407162	N63B55	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
75	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63831	dechahund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434082	A1373481	Hs.131715	hypothetical protein PRO1777	4.05
	443646	A1085198	Hs.164226	ESTs	4.05
	434265	AA845811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tra	4.05

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
	424176	AL137273	Hs.142307	hypothetical protein	4.04
5	452259	AA317439	Hs.28707	signal sequence receptor, gamma (transc	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	408666	V00495	Hs.184411	albumin	4.02
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
10	449446	D60730	Hs.57471	ESTs	4.00
	421037	AI634808	Hs.197653	gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	448310	AI480316		KIAA0628 gene product	4.00
	408155	AB014528	Hs.43133	plasminogen	3.98
15	413841	M34276	Hs.76576	NA	3.98
	400110	NA		matrix metalloproteinase 10 (stromelysin	3.97
	400289	X07820	Hs.2268	cyclin E1	3.97
	443715	AI563187	Hs.9700	DKFZP58G1517 protein	3.97
	408296	AI117452	Hs.44155	ESTs	3.97
20	450164	AI239923	Hs.30098	dopachrome tautomerase (dopachrome delta	3.95
	451592	A805416	Hs.213897	ESTs	3.95
	402373	AI135225	Hs.301865	ESTs	3.95
	426199	AA371685	Hs.97090	ESTs	3.95
	414148	BE084049		gb:MO-BT0651-270400-003-f02 BT0651 Homo	3.95
25	417006	AW673506	Hs.80758	aspartyl-tRNA synthetase	3.94
	449532	WT74653	Hs.271593	ESTs, Moderately similar to A47582 B-cell	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excise	3.93
	436281	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004665	Hs.127337	axin 2 (conductin, axil)	3.91
30	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
	443054	A1745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278481	matillin 3	3.90
	451229	AW967707	Hs.48473	ESTs	3.90
	413583	AI120806	Hs.5888	ESTs	3.90
35	437702	AW973953	Hs.293744	ESTs	3.90
	437207	T27503	Hs.15829	hypothetical protein FLJ142910	3.90
	434899	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fs, clone HE	3.90
	423697	BE088897	Hs.131834	Homo sapiens mRNA; cDNA DKFZp434B0328 (1	3.90
	428622	W28418	Hs.30715	potassium voltage-gated channel, Isk-related	3.90
40	432289	AI80145	Hs.55118	ESTs	3.89
	413304	NM_000401	Hs.75324	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11680 fs, clone HE	3.88
	410094	BE147697	Hs.58593	general transcription factor IIIF, polype	3.88
	441826	AW503603	Hs.129915	phosphotesterase related	3.87
45	440059	R69743	Hs.116774	Integrin, alpha 1	3.86
	428262	A1782141	Hs.195270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
50	448315	AW290912	Hs.20707	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69583	CDC6 (cell division cycle 6, S. cerevisi	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016870	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146086	ESTs	3.83
55	449508	AK001566	Hs.23818	hypothetical protein FLJ10704	3.82
	428227	AA321849	Hs.2248	small inducible cytokine subfamily B (Cyt	3.82
	435040	AB32350	Hs.152625	ESTs	3.81
	428249	F05422	Hs.168382	nucleoporin-like protein 1	3.81
60	451110	AI055040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
	437631	AA784749	Hs.287245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
65	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450096	AK682088	Hs.79375	holocarboxylase synthetase (biotin-1-prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
70	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thromboplast	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970572	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
	406667	M12523	Hs.184411	albumin	3.72
75	436411	AW67452		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI76098	Hs.21411	ESTs	3.72
	410564	NM_008033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fs, clone NT	3.70
	442881	AI023175	Hs.167022	ESTs	3.70
80	432255	AA831032	Hs.111670	ESTs, Highly similar to JC2257 prolyl o	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405480	NA		NA	3.70
	452624	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.69
5	444471	AB020584	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
10	417791	AW965339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.66
	430294	A1538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
15	420595	AA278865	Hs.88523	ESTs	3.65
	404477	NA	NA	NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.16536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
20	414463	T63078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
	457465	AW301344	Hs.122908	DNA replication factor	3.64
	438149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.268968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
25	424841	AB001106	Hs.151413	glia maturation factor, beta	3.63
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.62
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	426268	H09604	Hs.13268	ESTs	3.61
30	449722	BE280074	Hs.23980	cyclin B1	3.60
	426389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheli	3.60
	419945	AV280975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.82669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	3.60
	420685	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
35	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AAB05443	Hs.179909	hypothetical protein FLJ22095	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028992	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
40	418588	T85017	Hs.1192	KIAA0074 protein	3.59
	436981	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	NS9860	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
45	401165	NA	NA	NA	3.55
	415382	AI743539	Hs.72485	ESTs, Weakly similar to non-lane beta ga	3.55
	433668	AL157518	Hs.90421	PRO2453 protein	3.55
	421628	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
50	443325	BE398008	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethenol-	3.55
55	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 (s, clone NT	3.54
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	3.54
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.52
60	423441	R68649	Hs.278359	estatin in melanoma 1 like	3.51
	452940	AA025722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.50
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW309351	Hs.287955	Homo sapiens cDNA FLJ13090 (s, clone NT	3.48
	448915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.47
65	427975	AI536065	Hs.122460	ESTs	3.46
	400297	AI127078	Hs.334473	hypothetical protein DKFZp684O1278	3.45
	404253				3.45
	435587	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 (s, clone NT	3.45
	432158	W33165	Hs.22983	UDP-glucosidase/glycoprotein glucosyltransferse	3.45
	417315	AI080042	Hs.336901	ribosomal protein S24	3.45
	419140	AI982647	Hs.215725	ESTs	3.44
	446901	AI347274	Hs.19374	gb:tc05d02x1 NCI_CGAP_Co16 Homo sapiens	3.43
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
70	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.42
	442717	R88362	Hs.190591	ESTs, Weakly similar to T23976 hypothet	3.41
	443426	AF099158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.41167	ESTs	3.41
	430264	AA470518	Hs.200771	gb:nc071f10.s1 NCI_CGAP_Pr1 Homo sapiens	3.40
75	450158	AI702416	Hs.271400	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JCS795 CDEP prot	3.40
	444826	A1674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
80	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

418939	AW630803	Hs.89497	lamin B1	3.40	
418134	AA397769	Hs.86617	ESTs	3.40	
430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39	
5	427927	AI879165	CCAAT/enhancer binding protein (C/EBP),	3.39	
410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39	
410406	AI969703	Hs.1486	glycerol kinase	3.38	
408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38	
452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothet	3.38	
446432	AI377320	Hs.150058	ESTs	3.36	
10	456853	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PI.	3.35
425322	UG63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35	
428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35	
421039	NM_003478	Hs.101299	cullin 5	3.35	
15	407819	R42185	ESTs	3.35	
424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35	
433361	AW469373	Hs.300141	ribosomal protein L39	3.35	
435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35	
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35	
20	454018	AW016892	Hs.100855	ESTs	3.35
439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35	
453941	U39917	Hs.36920	Bloom syndrome	3.34	
411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33	
435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33	
25	438008	AA775026	Hs.203802	ESTs	3.33
421248	AW582962	Hs.102897	CGI-47 protein	3.33	
451707	AW051081	Hs.60973	ESTs	3.33	
457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31	
443613	A1079356	Hs.27774	gbv39b09.s1 Scores_NhIMPu_S1 Homo sapi	3.31	
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.31
438746	AI885816	Hs.184727	ESTs	3.30	
408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30	
427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (SSKD, Ze	3.30	
458855	AW361299	Hs.107000	hypothetical protein FLJ11294	3.30	
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30	
417720	AA205625	Hs.208057	ESTs	3.29	
428571	NM_005531	Hs.2291	Probe HTg737 (polycystic kidney disease,	3.29	
452862	AW378065	Hs.8687	ESTs	3.28	
40	414343	AL036166	coated vesicle membrane protein	3.28	
437222	AL117588	Hs.12778	ESTs	3.28	
422665	AJ011812	Hs.119018	transcription factor NRF	3.28	
414706	AW340125	Hs.76989	KIAA0097 gene product	3.28	
446865	D13767	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27	
447829	AI433029	Hs.164104	ESTs	3.27	
45	427576	BE242811	Hs.2173	fucose transferase 4 [alpha] fucoy	3.27
456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26	
407905	AA715284	Hs.240311	gbav36f03.r1 NCL_CGAP_Br5 Homo sapiens	3.26	
419741	NM_070709	Hs.93002	ubiquitin carrier protein E2-C	3.26	
50	424581	M62062	Hs.150917	cetarin (cadherin-associated protein), a	3.25
446592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothet	3.25	
453920	AW450240	Hs.257274	ESTs	3.25	
451797	AW663958	Hs.333513	small inducible cytokine subfamily E, me	3.25	
413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25	
55	410659	A1080175	Hs.68826	ESTs	3.25
446202	AI279706	Hs.149474	ESTs	3.25	
432193	AA372264	Hs.273103	hypothetical protein FLJ10706	3.25	
439262	AA832333	Hs.333045	ESTs	3.25	
401823	NA	NA	NA	3.25	
60	441264	AA927170	Hs.23290	ESTs	3.25
424061	NM_008413	Hs.139120	ribonuclease P (30kD)	3.24	
408321	AW405882	Hs.44205	cortistatin	3.24	
447432	AW968473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.24	
404519				3.24	
65	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
422660	AW297562	Hs.103267	hypothetical protein FLJ22548 similar to	3.23	
427951	AW238165	Hs.143134	ESTs	3.22	
427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22	
70	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21	
426472	BE246138	Hs.30853	ESTs	3.21	
410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21	
439979	AW600291	Hs.68623	hypothetical protein FLJ10430	3.21	
422363	T55979	Hs.115474	replication factor C (activator 1) 3 (3B	3.20	
75	443162	T49851	Hs.9029	DKFZP434G032 protein	3.20
431679	AW072372	Hs.287446	hypothetical protein FLJ11184	3.20	
430439	AI133561	Hs.241426	DKFZP434B061 protein	3.20	
407201	N31998	Hs.164256	hypothetical protein FLJ20557	3.20	
437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypothet	3.20	
80	434180	BE561196	Hs.114276	ESTs	3.20
407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20	
412966	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19	
414386	X00442	Hs.75990	haptoglobin	3.19	
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	3.18	

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889882	Hs.271826	ESTs, Weakly similar to I38022 hypothesis	3.17
5	429616	A1982722	Hs.120845	ESTs	3.17
	415083	A632683	Hs.27179	Homo sapiens cDNA FLJ12933 firs, clone NT	3.16
	424687	JG070	Hs.151738	matrix metalloproteinase 9 (gelatinase B)	3.16
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 firs, clone NT	3.16
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 firs, clone H	3.15
10	443830	A142095	Hs.143273	ESTs	3.15
	413516	BE145807		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 firs, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 firs, clone PL	3.15
15	427687	AW003867	Hs.1570	histamine receptor H1	3.15
	455058	A1807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.15
	441720	A1346487	Hs.28739	ESTs	3.15
	419569	A971651	Hs.91143	Jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
20	429857	AW204530	Hs.99500	ESTs	3.15
	403137				3.14
	425268	A1807883	Hs.180059	Homo sapiens cDNA FLJ20653 firs, clone KA	3.14
	428645	AA431400	Hs.98728	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 firs, clone C	3.14
	439277	R80051	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	A1807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406688	T62745	Hs.184411	albumin	3.13
	452194	A1694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 firs, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) t-	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE3448343, mRNA,	3.11
35	441790	AW294009	Hs.132208	ESTs	3.11
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU 6	3.10
	424602	AK002055	Hs.161046	hypothetical protein FLJ1193	3.10
40	402963				3.10
	428987	AW978441	Hs.2986100	ESTs	3.10
	455538	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
	428853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
45	417846	AI117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001852	Hs.59423	ATP-dependent RNA helicase	3.10
	421841	AA908187	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
	408353	BE439938	Hs.44298	mitochondrial ribosomal protein S17	3.10
50	433037	NM_014158	Hs.279938	HSPC057 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 firs, clone NT	3.09
	457726	A1217477	Hs.194591	ESTs	3.09
	415786	AW418198	Hs.257824	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axis 2 (conductin, exil)	3.08
	417601	NM_014738	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORT1	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119099	hypothetical protein FLJ12868	3.07
60	425851	NM_001490	Hs.159542	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 firs, clone H	3.07
	416402	NM_007115	Hs.1012	complement component 4-binding protein,	3.06
	436554	A1958510	Hs.301173	ESTs	3.06
	413801	M82246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA161342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.06
	474048	AW383080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Samf	3.05
70	406333				3.05
	428454	U55938	Hs.184376	synaptosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RC0-MT0013-2B0300-031-e03 MT0013 Homo	3.05
	458632	A174445	Hs.167073	Homo sapiens cDNA FLJ13047 firs, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
75	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypothesis	3.05
	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	A1761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, fetal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159625	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

419195	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04	
446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fs, clone H	3.03	
425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.02	
452834	AI538627	Hs.105685	KIAA1688 protein	3.02	
5	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fs, clone HE	3.02
	416568	Hs4844	Hs.138558	ESTs	3.02
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
10	412719	AW016610	Hs.129911	ESTs	3.01
	439586	AA922936	Hs.110039	ESTs	3.01
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (psc)	3.01
	429703	T33154	Hs.28705	ESTs	3.00
15	400296	A305627	Hs.139338	ATP-binding cassette, sub-family C (CFTR)	3.00
	415261	T40928	Hs.8346	ESTs	3.00
	419435	A200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
	429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
20	407182	AA312551	Hs.230157	ESTs	3.00
	424202	BE350295	Hs.15032	RAN binding protein 17	3.00
	445685	AW170015	Hs.6594	ESTs	3.00
	420552	AK000492	Hs.98808	hypothetical protein	3.00
25	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
	441928	A370188	Hs.211454	ESTs	3.00
	430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
	417895	A167277	Hs.183733	ESTs	3.00
30	447175	A385208	Hs.293608	ESTs	3.00
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	3.00
	435447	A1872932		gb:wm72e03.x1 NCI_CGAP_U12 Homo sapiens	3.00
	408394			gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.00
	454975	AWB48047		phosphatidylinositol binding clathrin as	3.00
35	441635	AL135735	Hs.7885	transcriptional intermediary factor 1	3.00
	428361	NM_015905	Hs.183858		3.00

35

TABLE 6B

	Pkey:	Unique Ecs probeset identifier number		
40	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
	Pkey	CAT number	Accession	
45	411785	125700_1	H43346 AA249302 AA095182	
	411864	1262055_1	AW948147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160	
	412359	123085_1	AW837985 AW837938 AA101955 AW837913 AW837935	
	413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856	
	414148	142133_1	BE084049 AW228007 AA135984	
50	424492	240008_1	AI133482 AI207619 AA241626	
	430264	315008_1	AA470519 BE303010 BE302854 BE384120	
	431084	327472_1	AI903735 AA491283 AI694953 AW976903 AA761352	
	433687	373051_1	AA743991 AA604982 AW272737	
	434414	38585_1	AI789376 S46400 AW811617 AW811618 W005657 BE142245 AW858232 AW861851 AW858362 AA232351 AA218967 AA055655 AW858231	
55			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199442 AA223384 AA227082 AA227080 T12379 AA092174 T61139	
			AA149776 AA699829 AW879180 AW813567 AW813539 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730	
			AA157715 AA053524 AW849581 AW854566 C05254 AW862836 T92537 AW812621 AA206583 AA209204 BE158909 AA226624 AW829309 AW8991957	
			N68951 AA527374 H66215 AA045584 AI694285 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659	
60	436447	406400_1	BE072932 AA652306 BE220163 WBB695 TB1307 H91447	
	436411	419334_1	AW674352 AA715374 Z220205	
	443613	575391_1	AI079356 W23207	
	446901	697809_1	AI347274 AW844024	
	448310	757918_1	AI480316 AW847535	
65	451401	868474_1	AI793183 AW875182 AW875178 AW875176	
	454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093	
	454975	1247077_1	AWB48047 AWB48202 AW846531 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AWB48069 AW848905	
	455838	1374605_1	AW848214	
70			BE145808 BE145807 BE181889	

70 TABLE 6C

	Pkey:	Unique number corresponding to an Ecs probeset		
75	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., <i>Nature</i> (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		

	Pkey	Ref	Strand	Nt_position
5	400534	6981826	Minus	278637-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401844	8576138	Plus	82055-83959
	401823	2262095	Minus	42575-42897,43189-43287,45030-45974
	402167	8571795	Plus	109122-110357
10	402963	5419653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770811	Minus	1414-1513,1624-1756
	404026	7341444	Plus	131740-131906
	404232	8218045	Minus	71800-71956
	404263	9367202	Minus	55675-56055
15	404477	8080699	Plus	113390-113577
	404516	8151957	Plus	114153-114322
	404519	8152000	Plus	12817-13000
	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37899-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405394	6624123	Minus	31900-32373
20	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49693-49850

30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
40	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
45	441031	AI110584	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1199 protein	49.18
	428930	L22524	Hs.2258	matrix metalloproteinase 7 (matrilysin, secreted frizzled-related protein 4	42.22
	421552	AF026692	Hs.105700	group-specific component (vitamin D bind	34.64
	429201	X03178	Hs.198246	Homo sapiens cDNA FLJ11041 fis, clone PL	33.38
50	452281	T93600	Hs.28792	ESTs	33.10
	447033	A357412	Hs.157601	Homo sapiens cDNA FLJ14814 fis, clone NT	31.24
	428839	A1767756	Hs.82302	AW075483	26.84
	438461	AW075483	Hs.286049	phosphoserine aminotransferase	25.40
	413841	M34276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
55	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21632 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415989	A1267700	Hs.317584	ESTs	20.92
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metap	19.22
	421470	R274936	Hs.1378	annexin A3	17.92
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
60	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AAD45673	Hs.22900	nuclear factor (erythroid-derived 2)-like	17.08
	421462	AF016495	Hs.104624	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30966	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gb:n21d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
65	433447	U29195	Hs.3281	neuronal pentrax II	16.59
	414386	X00442	Hs.75990	haptoglobin	16.19
	425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
	444764	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W78326		gb:zid60d04.r1 Scores_fetal_heart_NbHH19W	15.80
	443211	AI126388	Hs.143655	ESTs	15.78
70	439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414659	AV856184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412719	AW016610	Hs.129911	ESTs	15.24
	439451	AF086270	Hs.278654	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	cromomucoid 1	14.35
	441243	A1767055	Hs.193002	ESTs	14.30
5	413318	AU076607	Hs.75285	inter-alpha (globulin) Inhibitor, H2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428281	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AAB11244	Hs.164168	ESTs	13.40
10	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	13.00
	449199	AI990122	Hs.195988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
15	451561	NS2812	Hs.177403	ESTs	12.72
	420734	AW972872	Hs.293736	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	12.50
	441377	BE218239	Hs.202658	ESTs	12.45
	435981	H74318	Hs.188620	ESTs	12.38
20	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
	428684	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA869982	Hs.271826	ESTs, Weakly similar to I380222 hypothesis	12.34
	430290	A734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
	450528	AW382884	Hs.204716	ESTs	12.24
25	446232	AI2B1848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432882	AI623817	Hs.168457	ESTs	12.08
	407884	BE076316	Hs.95011	synophilin, beta 1 (dystrophin-associate	12.02
30	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	NS8172	Hs.109370	ESTs	11.94
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	11.68
	447532	AK000814	Hs.18791	hypothetical protein FLJ20507	11.57
35	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila)	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-Interacting pro	11.34
40	452803	AI953425	Hs.246911	ESTs, Weakly similar to I380222 hypothesis	11.32
	433011	H07960	Hs.306044	C9-05 protein	11.30
	423575	C1B863	Hs.163443	Homo sapiens cDNA FLJ11578 fis, clone HE	11.22
	455777	A5524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44080	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
45	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA260970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	10.68
50	440526	A1832243	Hs.211471	ESTs	10.63
	427644	A1767152	Hs.181400	ESTs, Weakly similar to I78885 serine/threonine kinase 6b3.1 Soares placenta Nb2HP Homo	10.62
	447974	R76886		gb:6464b03.s1 Soares placenta Nb2HP Homo	10.62
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	10.52
	453922	AF053308	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
55	457055	AI476318	Hs.192480	ESTs	10.40
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW5003756	Hs.286184	hypothetical protein dJ561D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447506	AL049268	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr)	10.28
	404567				10.14
60	428536	AI143139	Hs.2288	vitamin-like 1	10.08
	444391	BE367335	Hs.283713	ESTs, Weakly similar to S64054 hypothesis	10.05
	437267	AW511443	Hs.268110	ESTs	10.00
	420583	H77859	Hs.65450	retinol 4	10.00
65	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013989	Hs.164424	deiodinase, iodothyronine, type II	9.97
	449565	AI021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cDNA R76593	9.90
	434809			gb:60c11.1 Soares placenta Nb2HP Homo	9.90
70	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447863	AL047611	Hs.268885	Homo sapiens cDNA FLJ14248 fis, clone OV	9.84
	448106	A1800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
75	440581	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kyuureninase (L-kyuurenine hydroxylase)	9.36
	401742	NA		NA	9.30
80	416393	N54037	Hs.262669	plasminogen-like	9.28
	413339	A1B18080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	A1B08060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr)	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149796	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419968	X04430	Hs.93913	Interleukin 6 (interferon, beta 2)	9.16
5	413597	AW302886	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AV007519	Hs.104820	Homo sapiens cDNA FLJ13694 fts, clone PL	9.08
	450164	AI239923	Hs.30098	ESTs	8.95
10	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140396	Hs.21821	hypothetical protein DKFZp762D076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW838616		gb:RC5-LT0054-140200-013-D01 LT0054 Homo	8.90
15	419131	AA406293	Hs.41167	ESTs	8.86
	444783	AK001468	Hs.62160	anillin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
20	419762	AA249573	Hs.152818	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
	412446	AI768015	Hs.92127	ESTs	8.71
	433285	AW759544	Hs.237396	ESTs	8.68
	414536	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.76531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
25	430835	AI240006	Hs.192326	ESTs	8.60
	445467	AI239832	Hs.16817	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256462	Hs.2257	vitronectin (serum spreading factor, som	8.50
30	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA223056	Hs.191518	ESTs	8.42
35	445436	AI224105	Hs.151408	ESTs	8.38
	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen In mela	8.34
	425761	AW664214	Hs.195729	ESTs	8.33
	449419	R34910	Hs.119172	ESTs	8.29
40	407007	U22961		gb:Human mRNA clone with similarity to L	8.28
	420900	AL046633	Hs.44269	ESTs	8.25
	452503	AB000508	Hs.29736	TNF receptor-associated factor 5	8.23
	456242	BE299588	Hs.28465	Homo sapiens cDNA FLJ21869 fts, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:n76g11.s1 NCL_CGAP_Co3 Homo sapiens	8.16
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
	448155	AI532695	Hs.159422	Homo sapiens cDNA FLJ13997 fts, clone Y7	8.10
	418379	AA218940	Hs.137516	ridgefin-like 1	8.07
	424560	AA158727	Hs.160555	protein predicted by clone 23733	8.06
50	453116	AI276680	Hs.146086	ESTs	8.04
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
	409687	T51125	Hs.8493	ESTs	8.00
	407730	AI027274	Hs.268941	Homo sapiens cDNA FLJ14866 fts, clone PL	8.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37876	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-2ON2 o	7.98
	421633	AF121880	Hs.106260	splicing nuclein 10	7.92
	432542	AW083929	Hs.16088	claudin 2	7.86
	414869	AA157291	Hs.21479	ubrinuclein 1	7.84
60	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V0D485	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	438516	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fts, clone NT	7.77
	406360	NA		NA	7.76
65	406867	M31125	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112284	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N66045	Hs.133529	ESTs	7.70
	449870	AI672487	Hs.15423	hypothetical protein HDMC04P	7.64
70	426681	A8018297	Hs.158183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AI301918	Hs.334264	ESTs	7.60
	420807	AA280627	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fts, clone H	7.60
	410718	A1920783	Hs.191435	ESTs	7.60
75	430848	AW021726		gb:Z27e02_y1 Merton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 feni	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
	455997	AW937420	Hs.69662	ESTs	7.54
80	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50986	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445840	AW989626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	7.49
	404995				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433659	AW896758	Hs.273789	ESTs	7.44
	423552	AW877787	Hs.136102	KIAA0853 protein	7.44
	431193	AW749505	Hs.286770	KIAA1719 protein	7.43
5	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AO57052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
10	449347	AW649748	Hs.295901	KIAA0493 protein	7.34
	449444	AWB18436	Hs.23590	solute carrier family 16 (monocarboxylic prostaglandin beta 16	7.34
	447499	AW262580	Hs.147674	ESTs	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
15	445019	AK025540	Hs.281295	ESTs	7.28
	419474	AW988619	Hs.155849	ESTs	7.24
	417015	M3772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H4346	Hs.2346	gbyp05a04_r1 Scarce breast 3Nb1/Bst Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
	416143	AB056650	Hs.78033	glutamyl-peptide cyclotransferase (glu	7.18
20	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
25	443614	AV655396	Hs.7645	fibrinogen, B beta polypeptide	7.14
	448705	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	446480	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	A1377320	Hs.150058	ESTs	7.10
30	439295	AW205091	Hs.253536	ESTs	7.08
	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gbzw080c03.s1 Soares_Jesus_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
35	432435	BE218888	Hs.282070	ESTs	7.05
	427833	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
	446322	N23033	Hs.155814	ESTs	6.98
40	442577	AA292998	Hs.183900	ESTs	6.98
	429485	AF155627	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA446854	Hs.271004	ESTs, Weakly similar to 138022 hypothet	6.90
	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76635	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427678	C05768	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
	424402	M63108	Hs.1769	luteinizing hormone/chorionic gonadotropin r	6.86
	438394	BE375823	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AI133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020895	Hs.91662	KIAA0888 protein	6.80
55	451665	AA059246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	446501	A1302616	Hs.150819	ESTs	6.78
	442973	BE267665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydroxyimidase-like 2	6.76
60	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	protein convertase subtilisin/kexin I	6.72
	425478	AI007953	Hs.268840	ESTs	6.70
	411643	A1924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418556	A417215	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31864	frizzled (Drosophila) homolog 10	6.62
	433615	AT732982	Hs.269807	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001626	Hs.262445	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445181	AF046686	Hs.12593	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.22958	Homo sapiens clone IMAGE:451939, mRNA se	6.54
	432639	AW973785	Hs.586368	gb EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW830871	Hs.586368	squamous cell carcinoma antigen recogni	6.54
	449894	AK001578	Hs.24129	CLL7 protein	6.53
	442914	AW1BB551	Hs.993519	hypothetical protein FLJ14007	6.53
	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
75	441801	AW242799	Hs.86366	ESTs	6.52
	436542	AA687378	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.48
	436217	T53925	Hs.107	fibrogen-like 1	6.48
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.43
80	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2266	secretory granule, neuroendocrine protein	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma l1b	6.36
5	451369	N73222	Hs.279009	matrix Gla protein	6.36
	427899	AA829286	Hs.322053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	436532	AW291468	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AV298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99540	ESTs	6.32
	434032	AV008951	Hs.206892	ESTs	6.31
	444656	AI277824	Hs.145199	ESTs	6.30
15	433607	AA602004	Hs.23260	ESTs	6.26
	440659	AF134180	Hs.7327	claudin 1	6.25
	436663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
20	447500	AI381900	Hs.159212	ESTs	6.24
	407237	AA168872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone C17	6.20
	438138	R58299	Hs.177502	ESTs	6.20
25	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
	416857	AA188775	Hs.292453	ESTs	6.20
	427887	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fs, clone NT	6.18
	429698	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
30	438940	AF075045	Hs.271609	ESTs	6.18
	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
35	427513	AI476318	Hs.192480	ESTs	6.10
	448934	AI598134	Hs.225592	ESTs, Highly similar to T61145 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK002028	Hs.239881	hypothetical protein FLJ20275	6.08
	424856	AA347748	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
40	409048	H59980	Hs.37699	ESTs	6.08
	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33808	Hs.284176	transferrin	6.05
	453804	AA300204	Hs.35275	KIAA0852 protein	6.05
	442875	BE523003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	6.05
45	406243	Y00787	Hs.624	Interleukin 8	6.04
	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA883024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypoth	6.04
	407746	AK001952	Hs.38114	hypothetical protein FLJ11100	6.02
50	442116	AI84570	Hs.128813	ESTs	6.00
	423668	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30245	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
55	434739	AA804487	Hs.144130	ESTs	5.98
	449802	AW901604	Hs.23984	hypothetical protein FLJ20147	5.98
	420218	AW958037	Hs.288	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	ET4-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.159054	ESTs	5.94
60	439096	AA830185	Hs.269680	ESTs	5.94
	452608	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243988	nuclear autoantigenic sperm protein (his	5.94
	417246	AI760098	Hs.21410	ESTs	5.94
	433190	M25501	Hs.3210	renin	5.92
65	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AI791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
70	408887	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	carcinosomal P4.1-associated protein; unc	5.88
	450380	AI863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
	454853	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
75	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AI117588	Hs.12778	ESTs	5.86
	455530	AV655701	Hs.75183	cytochrome P450, subfamily IIIE (ethanol-	5.86
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
	409045	AA635062	Hs.60094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	5.84
80	441645	AI222279	Hs.201655	ESTs, Weakly similar to T23406 hypothet	5.84
	401352				5.84
	419088	AI538323	Hs.52620	Integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT	5.82
5	419220	AA811938	Hs.291759	ESTs	5.82
	438303	W00605	Hs.102784	ESTs	5.80
	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran diaphorase (Drosophila, homolog) 2	5.80
	429945	NM_006729	Hs.226483	ESTs	5.80
	438527	AW298119	Hs.202536	ESTs	5.78
10	435380	AA679001	Hs.192221	ESTs	5.78
	424086	A361010	Hs.102267	lysyl oxidase	5.76
	425898	AA365849	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428665	Hs.98563	ESTs	5.74
15	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fs, clone C	5.74
	413982	BE503035	Hs.278193	ESTs	5.74
	453240	AI696564	Hs.166254	hypothetical protein DKFZp566I133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
20	448986	AW372814	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
	433384	AI021992	Hs.124244	ESTs	5.70
	415385	R177798	Hs.7553	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
25	446665	NM_014953	Hs.323346	KIAA1008 protein	5.68
	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AM78463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
30	422805	AA438989	Hs.121017	H2A histone family, member A	5.62
	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	436777	AA825487	Hs.142179	ESTs	5.58
35	433849	BE465884	Hs.280728	ESTs	5.58
	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002778	Hs.89423	kelikrain 10	5.55
	435008	AF150262	Hs.152898	ESTs	5.55
	434184	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
	452881	AW135220	Hs.241921	ESTs	5.54
40	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
45	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
	417643	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434974	AA831878	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	Kinesin-like 1	5.50
	418882	NM_004998	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	404227	NA		NA	5.49
	412765	BE544476	Hs.54347	ESTs	5.49
	441708	AM66911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW185262		gb:zn67b05x1 NCI_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.89233	zinc finger protein	5.46
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437978	A1198823	Hs.150473	ESTs	5.44
	436007	AA737171	Hs.131809	ESTs	5.44
60	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452448	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187581	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	5.40
	441217	A192183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fs, clone CO	5.40
	453691	AB037751	Hs.30353	Homo sapiens mRNA full length Insert cDN	5.40
	408680	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	5.40
	433760	AA680003	Hs.109383	ESTs, Homo sapiens cDNA: FLJ23603 fs, clone L	5.39
70	446142	A1754693	Hs.145988	ESTs	5.38
	408562	AI345323	Hs.31141	Homo sapiens mRNA for KIAA1566 protein,	5.36
	433929	AI375499	Hs.27379	ESTs	5.36
	421153	H87879	Hs.102267	lysyl oxidase	5.34
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.34
75	453931	AI121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.259423	ESTs	5.33
	416067	A1927382	Hs.29857	ESTs	5.33
	438547	AA813118	Hs.163230	ESTs	5.32
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
80	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.30
	408522	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA			
	449508	AKD01566	Hs.23618	hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	5.28
5	417372	T39755	Hs.334728	ESTs	5.28
	443613	AU079356		gb:ox39609.s1 Soares_NhiMPu_S1 Homo sapi	5.28
	412610	X09098	Hs.74126	fatty acid binding protein 6, fetal (gas	5.27
	408943	NM_007070	Hs.49105	FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524	ESTs	5.26
	447982	H22953	Hs.137551	ESTs	5.26
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AU824009	Hs.44577	ESTs	5.24
	409582	R27430	Hs.271565	ESTs	5.24
15	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	5.23
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	5.23
	418661	NM_001949	Hs.1169	E2F transcription factor 3	5.22
	446271	D82484	Hs.330994	ESTs	5.22
	435905	AW997484	Hs.5003	KIAA0456 protein	5.21
20	434551	BE387162	Hs.280868	ESTs, Highly similar to A35661 DNA excis	5.21
	416245	NS9650	Hs.27252	ESTs	5.20
	436016	AA808465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278	KIAA1201 protein	5.20
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length Insert cDNA	5.20
25	424281	AA766243		gb:ox13b11.s1 NCL_CGAP_GCB1 Homo sapiens	5.20
	449138	AW294215	Hs.195531	ESTs	5.20
	449416	AI631016	Hs.248311	ESTs	5.20
	430092	AI821399	Hs.16614	ESTs	5.20
	436574	AW293527	Hs.128465	ESTs	5.18
30	433377	AT752713	Hs.43845	ESTs	5.18
	440987	AA911705	Hs.130229	ESTs	5.18
	426116	AA868729	Hs.144694	ESTs	5.18
	441928	AI370188	Hs.211454	ESTs	5.17
	432657	AA831815	Hs.270840	ESTs, Weakly similar to I788B5 serine/th	5.17
35	438011	BE466173	Hs.145695	splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722	interleukin 1, alpha	5.16
	433393	AF036564	Hs.98074	Itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810	ESTs	5.14
40	420170	U43374	Hs.856831	Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I788B5 serine/th	5.12
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.12
	440652	AI216751	Hs.143977	ESTs	5.12
	419706	C04649	Hs.77899	tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.11B76B	ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.11B699	hypothetical protein FLJ12989	5.11
	407624	AW157431	Hs.246941	ESTs	5.11
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.11
50	452465	AA610211	Hs.34244	ESTs	5.10
	442633	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	5.10
	448952	AI609595	Hs.208038	ESTs	5.10
	408170	AW204515	Hs.31835	ESTs	5.08
	424238	AA337401	Hs.137635	ESTs	5.07
55	421072	AZ216069	Hs.89113	ESTs	5.08
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.06
	423854	AI674253	Hs.35B28	ESTs	5.06
	436862	AI821940	Hs.284622	ESTs, Moderately similar to ALU8_HUMAN A	5.06
	436554	AI985810	Hs.301173	ESTs	5.06
60	433264	DB5782	Hs.3229	cysteine dioxygenase, type I	5.04
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	5.04
	412666	AI000116	Hs.74420	origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.00
65	418217	AS910847	Hs.13442	ESTs	5.00
	401480	NA		NA	5.00
	456179	H75490	Hs.271930	ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
75	Pkey	CAT number	Accession	
	408432	1058667_1	AW195262 R27868 AW811262	
	408690	107490_1	AW864542 AA056567 AW882724	
	411765	125700_1	H43346 AA248302 AA095182	
	414372	143909_1	AA143854 AW753140 AA213770 AW970865 AA569075 AA492132	
80	424281	237742_1	AA766243 AA338252 AA338213	

	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488065
5	432340	345248_1	AA534222 AA632632 TB1234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H80163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI079356 W23267
	447197	711623_1	R36075 AI366546 R36187
	447974	745643_1	R76886 AI453674 R77049
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543560_1	AF069478 AF089479 AF069460

TABLE 7C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., <i>Nature</i> (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	Nt_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
30	401714	6715702	Plus	96484-96681
	401742	2911728	Plus	64003-64147
	403432	9719511	Minus	68204-68392
	403776	7770511	Minus	1414-1513,1624-1756
35	404227	7838233	Minus	93110-93259
	404567	7248169	Minus	101320-101501
	404996	6007800	Plus	37993-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405360	9256107	Minus	7513-7673

40 Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

45 TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
50	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
55	421996	AW583807	Hs.1460	glucagon	0.0233
	425970	AK000072	Hs.227089	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0416
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	0.0584
	426651	AU076546	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0587
60	425820	AL049977	Hs.162209	claudin 8	0.0501
	431436	AA505035	Hs.195651	ESTs	0.0507
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
	442009	AI733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	rral, T-cell differentiation protein	0.0707
65	429050	XB1333	Hs.194777	neprin A, beta	0.0714
	427018	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
	446947	AF145747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429857	D13626	Hs.2465	KIAA0001 gene product; putative G-prote	0.0769
	443506	H10661	Hs.182124	ESTs, Weakly similar to I38022 hypothetical	0.0838
70	416314	N88802	Hs.5422	glycoprotein M63	0.0853
	451181	AI796330	Hs.207461	ESTs	0.0873
	429001	AF098851	Hs.194720	ATP-binding cassette, sub-family G (WHITE)	0.0888
	426835	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
	429350	AI754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

	411529	AA430348	Hs.317598	Homo sapiens cDNA FLJ12827 firs, clone NT	0.0951
	441066	AW205427	Hs.190725	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	Insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
5	433546	AJ075877	Hs.125461	hypothetical protein FLJ11539	0.1007
	415154	D63175		gb:HUM501B09B Clontech human placenta po	0.1032
	409321	AW8600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63597	Hs.2996	surase-isomallase	0.1107
10	430468	NM_004673	Hs.241519	angiopoletin-like 1	0.1114
	427167	AJ239507	Hs.99196	hypothetical protein MGC11324	0.1147
	441212	AW242447	Hs.146182	Cytosolic beta-glucuronidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 firs, clone H	0.1211
	412639	AW951284	Hs.296235	ESTs	0.1239
15	453399	Z70295	Hs.32956	guanylate cyclase activator 2B (uroguanylin)	0.1240
	403548				0.1248
	421913	AJ934365	Hs.109439	osteoglycan (osteolinductive factor, minre	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
20	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
	454790	AW820852		gb:RC2-ST0301-120200-011-112 ST0301 Homo	0.1328
25	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	laminin 1 (smooth muscle)	0.1395
30	436889	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
	404767				0.1460
	407286	AJ235864		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 firs, clone L	0.1463
35	452768	AW069459	Hs.61539	ESTs	0.1466
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
	414831	M31159	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:Hsaplens mRNA for CD58 T3 protein.	0.1466
	402076				0.1487
40	453500	AJ478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44565	ESTs	0.1500
	431706	AJ816088	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AJ824184	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	416390	AF133820	Hs.84665	ttn Immunoglobulin domain protein (myo	0.1529
	435056	AW023337	Hs.5422	glycoprotein M6B	0.1532
45	428034	AJ278989	Hs.66123	Homo sapiens cDNA FLJ13443 firs, clone PL	0.1538
	426609	AF062246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
50	425220	AW975317	Hs.162987	ESTs	0.1558
	445200	AA084460	Hs.12409	somatostatin	0.1558
	442328	T78886	Hs.284450	ESTs	0.1563
	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW157727	Hs.11873	ESTs	0.1605
	447261	NM_006591	Hs.17917	extracellular link domain-containing 1	0.1615
55	437734	AA653951	Hs.180284	ESTs	0.1637
	414290	AJ568801	Hs.71721	ESTs	0.1638
	416935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AJ365585	Hs.146246	ESTs	0.1660
	442496	RS5073	Hs.124130	ESTs	0.1676
60	450693	AW450461	Hs.203965	ESTs	0.1698
	420738	AJ263022	Hs.82204	ESTs	0.1718
	405385				0.1745
	404638				0.1751
65	427333	AF057797	Hs.178658	aquaporin 8	0.1757
	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421666	AL035250	Hs.1408	endothelin 3	0.1784
	452854	AA437031	Hs.14060	prokinectin 1 precursor	0.1795
70	408514				0.1805
	454186	BE141030		gb:MR0-HT0087-201099-002-b11 HT0087 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131468	Hs.23767	hypothetical protein FLJ12666	0.1812
	412474	AI791451		gb:nt50c09.y5 NCI_CGAP_Ov2 Homo sapiens	0.1812
	436008	AI078428	Hs.58785	ESTs	0.1820
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
75	410577	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000038	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
80	413714	AI560944	Hs.71428	ESTs	0.1845

	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fs, clone CO	0.1904
	436659	A217900	Hs.144464	ESTs	0.1906
10	447164	AF026941	Hs.17518	Homo sapiens ckg5 mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA428240	Hs.126083	ESTs	0.1942
	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fs, clone NT	0.1944
	434683	AW298724	Hs.202639	ESTs	0.1957
	421885	AA609911	Hs.109012	MAX dimerization protein	0.1957
	452786	R61362	Hs.106542	ESTs, Weakly similar to T09052 hypothetical	0.1969
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
20	437740	AAB10265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	418961	BE391476	Hs.80817	ribosomal protein S16	0.2041
25	401465				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M236	0.2049
	416231	H30333	Hs.165062	ESTs	0.2049
	401753				0.2050
	433430	AIB63735	Hs.186755	ESTs	0.2051
	432190	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
30	411644	H92064	Hs.278826	Arg/Abl-interacting protein ArgBP2	0.2059
	403957				0.2063
	435900	AI243036	Hs.16094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419956	AL137939	Hs.40096	ESTs	0.2090
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	428452	AW614271	Hs.121847	ESTs, Highly similar to AC006014 8 simil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI016777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
	437354	AA749215	Hs.291886	ESTs	0.2137
45	447734	A421412	Hs.163659	ESTs	0.2144
	424585	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188099	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 cm	0.2151
	401521				0.2157
50	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (0.2165
	401024				0.2171
	448402	AI793107	Hs.27078	ESTs	0.2179
	441083	BE562811		gb:801336446F1 NIH_MGC_44 Homo sapiens c	0.2185
55	417355	D13163	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.213923	ESTs	0.2193
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26586 hypothesis	0.2212
	405654				0.2217
60	415471	F09747	Hs.268707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA825499		gbaf69g08,r1 Soares_NhHMPu_S1 Homo sapi	0.2242
	427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
65	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:801276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	458395	Z30300	Hs.281935	ESTs	0.2257
	439039	A655707	Hs.48713	ESTs	0.2268
	433575	AA600175	Hs.39720	ESTs	0.2268
70	416035	H42314		gb:y09e02,s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	A1372588	Hs.8022	TUBA protein	0.2283
	437191	NM_006846	Hs.931555	serine protease inhibitor, Kazal type, 5	0.2289
	434839	A1743059	Hs.134736	ESTs	0.2294
75	435731	AA699581	Hs.186811	ESTs	0.2299
	400855				0.2304
	446294	AI284935		gb:gk55g09,x1 NCL_CGAP_Co8 Homo sapiens	0.2305
	414193	BE260060		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
	411514	AW860178		gb:l3-CT0219-271099-022-H12 CT0219 Homo	0.2315
80	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.25556	tumor necrosis factor receptor superfamily	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fs, clone PL	0.2320
	443482	AW188093	Hs.250385	ESTs	0.2326

	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	ABD02367	Hs.21365	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95296	ESTs	0.2347
5	409331	M36534	Hs.53973	vasoactive intestinal peptide	0.2351
	431094	AWB72276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
10	439731	AI853135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129805	ESTs	0.2412
15	447482	AB033069	Hs.18705	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
	454145	AA0465872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial center homolog 1	0.2424
	404070				0.2427
20	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379045	Hs.18705	gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
	412622	AW684708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
25	426724	AA393823	Hs.293616	ESTs	0.2444
	405073				0.2445
	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na+/K+ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
30	426886	AW500131	Hs.171763	CD22 antigen	0.2471
	427078	AI676062	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AAB84208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
35	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
	424648	AA344578		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2505
	408345	R93851	Hs.63063	ESTs	0.2506
40	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-related	0.2508
	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449833	R82252	Hs.108106	protein kinase (cAMP-dependent, catalytic	0.2515
45	459275	AI080913	Hs.333352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
	422743	BE204678	Hs.179598	ribosomal protein L3	0.2526
	459688	U72671	Hs.161250	Intercellular adhesion molecule 6, tetran	0.2532
	450880	AK002183	Hs.286885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2538
50	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F08972	Hs.27372	SMN non-receptor tyrosine kinase	0.2549
	440274	R24595	Hs.7122	scrapple responsive protein 1	0.2553
	430087	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
55	453982	AW014995	Hs.281080	ESTs	0.2569
	453988	AW450570	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE289427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	0.2580
60	422581	L07648	Hs.118830	MAX-interacting protein 1	0.2582
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
65	420321	D78761	Hs.98657	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
	437032	AW857372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628433	Hs.271298	ESTs, Weakly similar to I54374 gene NF2	0.2605
70	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1898	paraoxonase 1	0.2611
	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022520	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
75	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172226F1 NIH_MGC_16 Homo sapiens c	0.2660
80	402182				0.2661
	402610				0.2663
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667	
444209	A1753134	Hs.146494	ESTs	0.2668	
416022	X59950	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677	
416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681	
5	422909	AA533356	gb:n87f10.s1 NCI_CGAP_Pr10 Homo sapiens	0.2683	
412047	AA934589	Hs.49696	ESTs	0.2693	
426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703	
442236	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709	
402425				0.2710	
10	450545	AW135582	Hs.201767	ESTs	0.2710
417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725	
419850	F06844		gb:HSCTME091 normalized infant brain cDN	0.2727	
428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730	
441493	AW070446	Hs.127037	ESTs	0.2733	
15	413541	BE147036	gb:QV4-HT0222-091199-024-a10 HT0222 Homo	0.2733	
428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone C1T	0.2734	
455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740	
447809	AW207805	Hs.164230	ESTs, Highly similar to JC7286 3',5'-cyc	0.2740	
20	444195	AB002361	KIAA0353 protein	0.2743	
415160	T82802	Hs.10587	gb:yd38a04.r1 Soares fetal liver spleen	0.2747	
421623	N40850	Hs.28625	ESTs	0.2755	
434464	BE063921	Hs.295971	ESTs	0.2755	
414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7kd protein [0.2756	
430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762	
25	432018	AA524447	Hs.152377	ESTs	0.2763
422854	AW998805		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768	
416397	H53035	Hs.337620	Homo sapiens AFG3L1 Isoform 1 mRNA, part	0.2775	
442420	AI024634	Hs.131729	ESTs	0.2775	
410850	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778	
30	427114	A1219896	Hs.97502	ESTs	0.2778
448466	AI522109	Hs.171066	ESTs	0.2778	
434445	A1349306	Hs.11782	ESTs	0.2784	
457115	A4A20712		gb:nc63c07.s1 NCI_CGAP_Pr1 Homo sapiens	0.2785	
459511	A1142379		gb:gg64c01.r1 Soares_fetals_NHT Homo sep	0.2786	
35	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
433633	A1880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799	
440236	AW996722	Hs.125297	ESTs	0.2799	
405691				0.2804	
405334				0.2804	
40	403047			0.2809	
412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809	
441042	AA077736		gb:7848A07 Chromosome 7 Fetal Brain cDNA	0.2815	
434650	AA764768	Hs.121158	hypothetical protein DKFZp14J0113	0.2816	
444453	AW379394	Hs.145126	ESTs	0.2817	
45	457736	AK000390	hypothetical protein FLJ20124	0.2820	
454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821	
427448	BE248449	Hs.2157	Wiskott-Artif syndrome (eczema-thromo	0.2822	
419564	U08988	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827	
438021	AA922192	Hs.54709	ESTs	0.2828	
50	413344	A48024	Hs.75302	myotubular myopathy 1	0.2837
447787	BE620108		gb:801483016F1 NIH_MGC_59 Homo sapiens c	0.2840	
457290	AA466293	Hs.105059	ESTs	0.2841	
458244	A1929453	Hs.122469	Homo sapiens cDNA FLJ13289 fis, clone OV	0.2841	
55	437483	AL390174	gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842	
407838	AA905097	Hs.85050	phospholamban	0.2845	
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846	
428212	AW444451	Hs.134812	ESTs	0.2853	
424433	H04607	Hs.9218	ESTs	0.2857	
60	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
404769				0.2863	
411620	AW854536		gb:RC3-CT0255-200100-024-a08 CT0255 Homo	0.2868	
428746	AW503820	Hs.192861	Spl-B transcription factor (Spl-1/PU.1)	0.2870	
431822	AA516049		gb:np66d01.s1 NCI_CGAP_Lip2 Homo sapiens	0.2872	
65	441290	W27501	cholinergic receptor, nicotinic, alpha p	0.2874	
422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877	
421935	AA131632	Hs.109572	CMP-NeuAc2(beta)-N-acetylgalactosamine	0.2878	
447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880	
405364				0.2881	
70	422165	AL041199	Hs.1481	histidine decarboxylase	0.2892
431087	H12723	Hs.290791	ESTs	0.2892	
450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2892	
445627	AW818475	Hs.7363	ESTs	0.2893	
436144	AW881250	Hs.148387	ESTs	0.2896	
445152	A1214657	Hs.283597	EGTs	0.2891	
75	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 f	0.2891
455614	AI693369	Hs.202274	ESTs	0.2899	
419683	AA248897	Hs.48784	ESTs	0.2900	
411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904	
80	430770	AA766694	Hs.123298	ESTs	0.2913
444459	A1680524	Hs.148876	ESTs	0.2913	
444918	A1202262	Hs.283362	ESTs	0.2915	
410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915	
435598	AA609470	Hs.163026	ESTs	0.2921	

413056	BE063031	gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
443998	AI620661	Hs.296276 ESTs	0.2924
424412	H15512	Hs.10043 hypothetical protein FLJ13074	0.2925
421204	AW081587	Hs.165051 ESTs	0.2928
5	420831	AF044197 Hs.100431 small inducible cytokine B subfamily (Cy	0.2938
	440507	glob1b07.r1 Scores infant brain 1NIB H	0.2943
	445555	AW974013 Hs.260809 ESTs	0.2945
	438570	Hs.84298 CD74 antigen (invariant polypeptide of m	0.2948
10	447195	T73745 Hs.279870 ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416 Hs.126177 Homo sapiens mRNA; cDNA DKFZp434O192 [fr	0.2956
	421920	Hs.1438 gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091 Hs.73734 glycoprotein V (platelet)	0.2959
	428042	Hs.76391 myxovirus (influenza) resistance 1, homo	0.2959
15	433745	AA419529 Hs.28980 hypothetical protein FLJ14540	0.2969
	417935	AF075320 Hs.28980 ESTs	0.2970
	420674	NM_000055 Hs.1327 butyrylcholinesterase	0.2973
	413537	BE146866 ESTs	0.2973
	445194	AI215867 Hs.175044 ESTs	0.2974
20	454135	AW135965 Hs.246783 ESTs	0.2976
	403418		0.2986
	457605	AV857778 Hs.3314 selenoprotein P, plasma, 1	0.2989
	408895	AI610447 Hs.48778 riban protein	0.2993
	448542	BE256176 Hs.278712 eukaryotic translation initiation factor	0.2994
25	417945	R29072 Hs.278712 gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637 Hs.173739 hypothetical protein FLJ10287	0.2996
	424566	M16801 Hs.1790 nuclear receptor subfamily 3, group C, m	0.2997
	430778	D90337 Hs.247916 naturetic peptide precursor C	0.3000
	451531	AA016311 Hs.114762 ESTs	0.3003
30	444926	AI202492 Hs.212933 ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407368	AF026942 Hs.208179 gb:Homo sapiens cig33 mRNA, partial sequ	0.3012
	459456	AA486036 Hs.190124 ESTs	0.3012
	417111	AW016321 Hs.82306 dastrin (actin depolymerizing factor)	0.3012
	452975	M85521 Hs.244482 Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
35	451959	AA056203 Hs.27337 hypothetical protein FLJ20623	0.3012
	410482	AW772187 Hs.191859 ESTs	0.3013
	417700	M36542 Hs.1101 POU domain, class 2, transcription facto	0.3018
	404414		0.3019
	432247	AA531287 Hs.105805 ESTs	0.3023
40	453471	AI037887 Hs.208179 ESTs	0.3028
	417481	AA203281 Hs.21798 ESTs	0.3029
	432306	Y18207 Hs.303090 protein phosphatase 1, regulatory subunit	0.3032
	448744	AL135424 Hs.9469 pleckstrin homology domain-containing, f	0.3033
	429223	BE284152 Hs.221994 ESTs	0.3034
45	404501	AW247252 Hs.75514 nucleoside phosphorylase	0.3037
	408829	AW419128 Hs.84298 CD74 antigen (invariant polypeptide of m	0.3039
	439839	AW257945 Hs.128490 ESTs	0.3039
	431848	AI378857 Hs.128758 ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706 Hs.89751 membrane-spanning 4-domains, subfamily A	0.3045
50	458789	AL157468 Hs.325625 Homo sapiens cDNA FLJ20848 fls, clone AD	0.3048
	443284	AI733625 Hs.133053 ESTs	0.3050
	447023	AA356764 Hs.17109 Integral membrane protein 2A	0.3052
	456583	AI479546 Hs.157081 hypothetical protein MGC4170	0.3055
	414567	BE281057 Hs.184519 hypothetical protein FLJ12949	0.3057
55	445123	AI762911 Hs.145369 ESTs	0.3064
	412882	AW963772 Hs.117772 gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3066
	434361	AF129755 Hs.117772 ESTs	0.3071
	414026	BE241713 Hs.117772 gb:TCAAP1E0472 Pediatric acute myelogenous	0.3072
	432149	AW814326 Hs.157022 ESTs, Weakly similar to T34549 probable	0.3073
60	408350	AW183350 Hs.260127 ESTs	0.3074
	401042		0.3077
	422588	AA312704 Hs.59457 hypothetical protein FLJ22127	0.3077
	438692	AB007950 Hs.6360 KIAA0481 gene product	0.3077
	447452	BE618268 Hs.102480 Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
65	444414	AW293214 Hs.8752 transmembrane protein 4	0.3085
	422373	AK001843 Hs.115700 Homo sapiens cDNA: FLJ23515 fls, clone L	0.3088
	430410	AF089144 Hs.250700 tryptase beta 1	0.3090
	419299	AI311085 Hs.62406 hypothetical protein FLJ22573	0.3091
	406672		0.3094
70	444010	AW976457 Hs.262867 ESTs	0.3098
	451699	AI118571 Hs.121667 ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3098
	432471	BE244667 Hs.296155 CGI-100 protein	0.3105
	405277		0.3106
	456765	AI497900 Hs.33057 ESTs	0.3108
	452090	AA022684 Hs.124573 Homo sapiens cDNA FLJ11477 fls, clone HE	0.3106
75	426497	AA379913 gb:EST92607 Skin tumor I Homo sapiens cD	0.3106
	406582		0.3106
	423621	BE002904 Hs.86379 gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
	417919	AI928203 Hs.86379 ESTs	0.3110
	414484	BE314385 gb:801154649F1 NIH_MGC_19 Homo sapiens c	0.3110
80	457439	AW410408 Hs.271167 L-pipecolic acid oxidase	0.3116
	426449	AI134009 Hs.169935 Homo sapiens mRNA; cDNA DKFZp58B6N1916 (f	0.3116
	419942	U25138 Hs.93841 potassium large conductance calcium-acti	0.3119
	458544	AI631036 Hs.195843 ESTs	0.3119

447778	BE620592	Hs.71190	ESTs, Weakly similar to S18508 hypothetical	0.3121	
449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospho	0.3125	
429338	AW170691	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125	
5	451385	AA017656	gb:ze39hh01_r1 Scores retina N2b4HR Homo	0.3125	
	446404	AA019561	LOC50627	0.3130	
	446516	R65984	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132	
	409404	BE220053	ESTs	0.3135	
10	417318	AW853937	ESTs	0.3139	
	443980	AI459140	ESTs	0.3140	
	459136	AI903291	gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142	
	414807	AI738916	hydroxyprostaglandin dehydrogenase 15-N	0.3143	
	434704	AW135276	ESTs	0.3143	
15	414214	D49958	glycoprotein M6A	0.3145	
	446378	AI905899	citrate synthase	0.3145	
	459233	AII939966	gb:MR0-CT0015-160799-002-b08 CT0015 Homo	0.3146	
	428193	NM_004235	Kruppel-like factor 4 (yut)	0.3148	
20	426515	BE394222	Homo sapiens, Similar to hypothetical pr	0.3150	
	426597	AA3B2250	ESTs	0.3153	
	459729	AL037285	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157	
	405071			0.3160	
	407457	AJ242724	gb:Homo sapiens mRNA for partial putativ	0.3162	
	403922	AW505582	KIAA1575 protein	0.3172	
	438219	AI916151	ESTs	0.3173	
25	412944	AA384110	ESTs	0.3175	
	431103	MS7399	Hs.44	0.3178	
	426662	AA879474	pleiotrophin (heparin binding growth fac	0.3178	
	444391	AI137597	hypothetical protein DJ1181N3.1	0.3178	
	432168	AK000563	hypothetical protein FLJ20556	0.3181	
30	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	0.3183	
	425367	BE271188	tein tyrosine phosphatase, receptor t	0.3185	
	448812	H30776	BM89 antigen	0.3188	
	411288	AW835511	gb:QV0-L70015-180200-127-d02 L70015 Homo	0.3189	
	422884	AW860976	ESTs	0.3190	
35	405535			0.3195	
	458663	AV658444	tankyrase, TRF1-interacting enoyl-rlta	0.3195	
	455353	W26786	gb:15d7 Human retina cDNA randomly prime	0.3195	
	414540	BE379050	Homo sapiens, clone MGCC10782, mRNA, com	0.3195	
	428558	AC004755	Homo sapiens chromosome 19, fosmid 37502	0.3195	
40	428106	BE620016	PTD010 protein	0.3198	
	411856	H67899	Homo sapiens cDNA: FLJ23269 fs, clone C	0.3202	
	445562	AW378397	gb:RC3-HTD220-031299-012-g06 HTD220 Homo	0.3205	
	437558	A1954795	ESTs	0.3205	
	448943	AI608810	ESTs	0.3205	
45	431999	AI133573	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207	
	419279	AA235900	ESTs	0.3208	
	405913			0.3209	
	425363	D83407	Down syndrome critical region gene 1-lik	0.3212	
	424729	AF069012	heart and neural crest derivatives expre	0.3212	
50	446020	AI480204	ESTs	0.3213	
	428082	AI135682	Homo sapiens mRNA for KIAA1737 protein,	0.3215	
	433663	AF083131	CATX-15 protein	0.3215	
	400641			0.3216	
	408140			0.3216	
55	415280	R56473	Hs.268715	ESTs	0.3217
	447635	AI669669	Hs.195362	ESTs	0.3217
	401887			0.3217	
	400767			0.3221	
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
60	448758	AB018311	Hs.21817	KIAA0768 protein	0.3222
	444780	AW242584	Hs.243823	ESTs	0.3223
	411466	AW847689	gb:IL3-CT0213-280100-058-G10 CT0213 Homo	0.3226	
	432749	NM_014438	Hs.278909	Interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
65	433234	AB040928	Hs.65366	KIAA1495 protein	0.3231
	422831	R02504	Hs.332843	ESTs	0.3234
	403215			0.3236	
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypothetical	0.3236
	446901	AI347274	gb:tb05d02x1 NCL_CGAP_Co16 Homo sapiens	0.3242	
70	430553	AW392821	gb:CM4-ST0276-021299-053-h09 ST0275 Homo	0.3254	
	446848	AI774824	Hs.13377	Homo sapiens clone 23849 and 23755 unkno	0.3257
	441143	AI027604	Hs.159650	ESTs	0.3257
	405138			0.3262	
	412888	M88151	gb:EST02579 Hippocampus, Striagene (cat	0.3262	
75	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.270840	ESTs	0.3263
	416426	AI180256	Hs.210473	Homo sapiens cDNA FLJ14872 fs, clone PL	0.3263
	423512	AW844694	Hs.305762	Homo sapiens cDNA: FLJ21391 fs, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
80	431851	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3267
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768863	Hs.134478	ESTs	0.3269
	451096	BE383234	Hs.25925	Homo sapiens, clone MGCC15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

454947	AW846590	gb:QV0-CT0180-011089-025-d07	CT0180 Homo	0.3275	
413814	BE169692	gb:PM1-HT0527-290200-006-a05	HT0527 Homo	0.3275	
422818	AA404290	Hs.97048	ESTs	0.3277	
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.3278	
5	414002	NM_006732	FBJ murine osteosarcoma viral oncogene li	0.3278	
452164	AB653711	Hs.75678	gb:t24b02X1 NCL_CGAP_Bm52 Homo sapien	0.3279	
458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated)	0.3279	
433197	AB040889	Hs.261022	KIAA1456 protein	0.3280	
10	405701			0.3282	
437782	AI370876	Hs.79090	exoplin 1 (CRM1, yeast, homolog)	0.3284	
459001	AT761313	Hs.204605	ESTs	0.3286	
422703	AA598956	Hs.120439	althanolamine kinase	0.3289	
417036	AF039918	Hs.80975	ectonucleoside triphosphate diphosphohyd	0.3290	
15	456041	BE270795	ESTs	0.3295	
423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296	
427630	AA405093	Hs.126519	ESTs	0.3296	
420172	AA601122	Hs.95655	secreted and transmembrane 1	0.3297	
445610	AB31648	Hs.143993	ESTs	0.3297	
20	411328	AW837083	gb:QV1-LT0037-160200-089-g08	LT0037 Homo	0.3300

Table B8

25	Pkey:	Unique Eca probeset identifier number			
CAT number:	Gene cluster number				
Accession:	Genbank accession numbers				
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30	Pkey	CAT number	Accession		
409921	1169516_1	AW600239 AW600255 AW505332			
410626	1212621_1	BE407727			
410845	1223881_1	AW807162 AW807328 AW807063 AW807183 AW807192 AW807033 AW807051 AW807288 AW807097 AW807270 AW807372 AW807280 AW807283			
410950	1227728_1	AW811633 AW811652 AW811888			
411288	1237709_1	AW835511 AW835517 AW835513			
411319	1238595_1	BES37094 AW836542			
411328	1238987_1	AW837063 AW935882 AW935957			
411456	1246771_1	AW847662 AW847667 BE145799			
411514	1248638_1	AW850178 AW850233 AW850445 AW850446			
40	411620	1252014_1	AW854536 AW854447 AW864495 AW854355		
411880	1263110_1	AW872477 BE088101 T05990			
412474	128869_1	AI791451 AI791288 BE019234 BE295601 AA111939			
412506	1301336_1	AW937199 H09337 T75143			
412682	1321572_1	AW983772 AW983730 AW983769 AW983836 AW983835 AW983837			
45	412888	1334784_1	M88151 BE061884 BE061883 BE061898 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061886 BE007474 BE007481 BE007533		
413056	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072			
413537	1375441_1	BE140866 BE146885 BE146867			
413541	1375449_1	BE147036 BE146951 BE146958 BE146966 BE146976 BE146955			
50	413814	1391574_1	BE169692 BE169421		
414026	1411109_1	BE241713 BE241912			
414193	1424706_2	BE260089			
414349	1437515_1	BE512966			
414484	1452830_1	BE314385			
55	414539	1460320_1	BE378046 BE395459		
415154	1525577_1	D63176 D78984 D63269			
415160	1525766_1	T82802 D78570 R08505			
416035	1567254_1	H42314 H42080 H45217 H15384			
417945	1711126_1	R29072 R29717 R2899 R29708 R29751 R29609 R29608 R29718 R29507 R29591 R29683 R29575 R28913 R28910			
419850	188485_1	FD6844 F06845 Z45488 AW748501 AW748591 AW752021 AW748545 AW853362 AW853363 AW853427 AA251253			
60	422909	222658_1	AA633355 AW848427 R67738 AA778031 AA614088 AJ823404 AA318991 AA720986		
422954	223239_1	AW998605 AW993131 BE514709 AA319445			
423621	230314_1	BE002904 H64890 AA320679			
65	424648	241947_1	AA344576 AA732430 AA344601		
426132	261431_1	AA370501 AW952704 AA370727			
426497	268121_1	AA379913 AA379981 AW9633523			
430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW803156 BE186656 AW821728			
431822	338082_1	AA516049 AW04922			
70	434098	380008_1	AA625499 AA625268 AA625184		
437483	43756_1	AL390174 AW898817			
440507	495677_1	HO6994 BE147998			
441042	50823_1	AA077736 AA078506 BE562497 Z17859			
441083	50904_1	BE562611 AA436054			
75	445682	647580_1	AW378397 AW378390 AW378358 AI247857		
446294	670076_1	AI284935 AW409822 BE408182			
446901	697809_1	AI347274 AW844024			
447787	73719_1	BE820108 BE312062 AW896316 BE262548			
451385	86787_1	AA017856 AA017374 AA019761			
452164	902091_1	AI863171 BE047919			
80	454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 BE141749 AW177598		

454790 1234752_1 AW820852 AW820773 AW821088
 454947 1245953_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
 455353 1284289_1 W26786 AW998612 AW902272
 5 457115 286601_1 AA420712 AA469165 AA420737
 459138 918860_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903345
 459233 944881_1 AI939966 AI939986 AI939951 AI939981 AI939976 AI939959

Table 8C

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Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I, et al., *Nature* (1999) 402:489-496.
 15 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
20	400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
	400641	8117693	Plus	4786-4932
	400672	8118724	Minus	148057-148603
	400767	8131627	Minus	80531-80629,82169-82278
25	400885	1945037	Minus	44462-45526
	401024	8117489	Plus	60551-60802
	401042	8117811	Plus	151364-151606
	401371	9560802	Plus	80801-81283
	401381	8570226	Minus	118629-119146,119392-119557
30	401485	6682292	Plus	25676-25800
	401521	7705251	Plus	9127-9234
	401763	8838183	Minus	155287-155529,159719-159997
	401776	9968323	Plus	115535-115743,117746-117839,120290-120455
	401887	7229981	Plus	93973-94120
35	401974	3126777	Plus	85330-85683
	402076	8117410	Plus	128316-128627
	402182	8575917	Minus	98298-98439
	402425	9796347	Minus	50224-50395
	402610	9926549	Minus	22955-23124
40	402895	8569671	Minus	159927-160055
	403047	3540153	Minus	59793-59968
	403215	7630945	Minus	177270-177971
	403418	6662692	Minus	176202-176395
	403548	8081591	Minus	38760-39352
45	403857	8076835	Minus	81649-81754
	404070	2996642	Plus	7210-7414,10043-10195
	404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
	404414	7382165	Plus	143127-143398
	404605	8212566	Plus	125032-125291
50	404638	9795751	Minus	99433-99528,100035-100161
	404698	9800109	Minus	60037-60144,62675-63081
	404767	7828287	Minus	23244-23759
	404789	8089713	Minus	175801-176823
	404927	7342002	Plus	68690-69563
55	404958	7407941	Minus	2731-4531
	405071	7708797	Minus	11115-11552
	405073	7769521	Plus	31419-31774
	405138	8576241	Plus	90303-90516
	405277	3980473	Plus	23471-23572
60	405282	3810573	Minus	10482-10689
	405334	3135285	Plus	139386-139856
	405364	2281075	Minus	48325-48491,49135-49252
	405386	8552772	Plus	48332-48454
	405535	97856583	Plus	63384-63545
65	405610	5757553	Minus	71907-72080
	405654	4895155	Minus	53624-53759
	405691	4508112	Plus	171360-171739
	405701	4283751	Plus	83243-83384
	405880	6758747	Minus	55573-56287
70	405913	7712139	Minus	7484-7678
	406140	9168231	Minus	49887-50219
	406592	4567182	Plus	352560-352963

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Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu3 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific

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background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

	Pkey:	Unique Ets probeset identifier number	ExAccn:	Exemplar Accession number, Genbank accession number	UnigeneID:	Unigene number	Unigene Title: Unigene gene title	R1:	90 th percentile of tumor samples divided by the 70 th percentile of normal body tissue samples, where the 15 th percentile of normal body tissues was subtracted from the numerator and denominator
5									
10									
15	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosidase, beta 1, 4-sialidase				29.34	
	406690	M29540	Hs.220529	(focuslink)NM_004363:Homo sapiens carcinogen, B betaine				25.56	
	406657	M12523						20.28	
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP)				18.84	
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel, ClC-3				17.38	
20	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating islet				16.99	
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestinal				16.61	
	431812	AI660552	Hs.356183	NM_356183:ESTs, Weakly similar to S3B4_H				16.42	
	437935	AW939591	Hs.5940	NM_030493:Homo sapiens mucin 13, epithelial				15.92	
	407242	M18728		(focuslink)NM_002483:Homo sapiens carcinogen, B betaine				15.84	
25	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease I				15.59	
	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B betaine				15.02	
	408685	M18728		(focuslink)NM_002483:Homo sapiens carcinogen, B betaine				14.54	
	422578	AF239566	Hs.1545	NM_001804:Homo sapiens caudal type homeobox protein 13				13.68	
30	423542	AW903920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)				13.23	
	421341	AI243212	Hs.374281	NM_007329:Homo sapiens deleted in malignancy 1				13.21	
	453863	X02544	Hs.572	Hs.572:orosomucoid 1				13.06	
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1				12.35	
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1				12.11	
	422260	AA315983	Hs.105484	NM_032044:Homo sapiens regenerating gene				11.99	
35	418888	AU076801	Hs.88436	NM_004063:Homo sapiens cadherin 17, Linc				11.87	
	407243	AA058357	Hs.74466	(focuslink)NM_006890:Homo sapiens carcinogen, B betaine				11.81	
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33				11.27	
	414463	T89078	Hs.78177	NM_001633:Homo sapiens alpha-1-microglobulin, Lefl				11.18	
40	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mRNA				10.82	
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible cation channel protein, Linc				10.73	
	450685	I15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso				10.57	
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metalloproteinase 1				10.39	
	423673	BE030364	Hs.1695	NM_002426:Homo sapiens matrix metalloproteinase 1				10.10	
45	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier family 16 (SCLC16A1)				9.91	
	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunoglobulin receptor				9.68	
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical protein				9.44	
	421100	AW351839	Hs.124660	NM_124660:ESTs, Moderately similar to 21				9.38	
	406741	AA058357	Hs.74466	(focuslink)NM_006890:Homo sapiens carcinogen, B betaine				9.34	
50	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (MPR1)				9.18	
	422281	M36803	Hs.346935	NM_000513:Homo sapiens hemopexin (HXP)				9.06	
	406687	M31126	Hs.352054	NM_352054:pregnancy specific beta-1-glycoprotein				9.02	
	409153	W03754	Hs.50813	NM_017625:Homo sapiens integrin (ITLN)				8.89	
	424887	J05070	Hs.151738	NM_004994:Homo sapiens matrix metalloproteinase 1				8.53	
55	422684	AA315933	Hs.120879	NM_120879:Homo sapiens clone MGC:32871				8.23	
	452204	AA025386	Hs.61311	NM_61311:ESTs, Weakly similar to S10590				8.10	
	430669	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I converting enzyme				8.05	
	413881	L00190	Hs.75599	(focuslink)NM_000498:Homo sapiens cerine				7.96	
	406399							7.73	
60	422424	AI186431	Hs.296638	NM_296638:prostate differentiation factor				7.71	
	428470	AC002301	Hs.184507	NM_184507:Homo sapiens, similar to Homol				7.43	
	417931	W95842	Hs.82861	NM_82861:Homo sapiens, clone MGC:22588				7.40	
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor				7.29	
	430272	X04898	Hs.237658	NM_237658:apolipoprotein A-II				7.25	
65	451917	AW391351	Hs.60820	NM_50820:hypothetical cardiac/skeletal m				7.21	
	421907	BE018556	Hs.109359	NM_109359:ATPase, Class V, type 10B				7.19	
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with sequence similarity 1				7.18	
	452594	AU076405	Hs.29981	NM_29981:solute carrier family 26 (sulfate)				7.03	
	424328	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysyl				7.00	
	443428	AF098158	Hs.9329	(focuslink)NM_012112:Homo sapiens chromo				6.92	
70	452194	AI694413	Hs.373599	NM_373599:EST				6.88	
	411975	A1916058	Hs.144583	NM_144583:Homo sapiens, clone IMAGE:3462				6.76	
	408243	Y00767	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL				6.59	
	422310	A3316622	Hs.98370	(focuslink)NM_030622:Homo sapiens cyclophilin A				6.55	
	431330	XG9532	Hs.2777	NM_022215:Homo sapiens inter-alpha (globulin)				6.53	
75	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protein				6.49	
	422330	D30783	Hs.115283	NM_001432:Homo sapiens epiregulin (EREG)				6.33	
	412104	AW205197	Hs.240951	(focuslink)NM_033120:Homo sapiens naked				6.31	
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plasmin 1 (Pls)				6.30	
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphatase 1				6.29	
80	430877	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG)				6.28	
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheobronchial				6.27	
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple helix				6.26	
	409532	W74001	Hs.55279	NM_002639:Homo sapiens cerine (or cysteine)				6.23	

417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23	
413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cyste)	6.23	
422527	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19	
5	411925	AK000334	NM_017767:Homo sapiens solute carrier fa	6.17	
	446921	AB012113	NM_002988:Homo sapiens small inducible c	6.17	
	415214	A1445236	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.17	
	414816	Y13709	NM_001265:Homo sapiens caudal type homeo	6.16	
10	422106	D84239	NM_003890:Homo sapiens IgG Fc binding pr	6.14	
	423803	NM_005709	{locuslink}NM_005709:Homo sapiens PDZ-73	6.13	
	452281	T93500	Hs.28792:Homo sapiens cDNA FLJ11041 fits	6.09	
	473432	A1199268	Hs.19322:Homo sapiens, Similar to RIKEN	6.02	
	443957	AA521049	Hs.353013:chromosome 20 open reading fra	5.96	
	403220			5.90	
15	408908	BE296227	Hs.250822	{locuslink}NM_003158:Homo sapiens serine	5.88
	449722	BE260074	Hs.23960	Hs.23960:cyclin B1	5.87
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	5.79
	414617	AJ39520	Hs.288817	{locuslink}NM_025130:Homo sapiens hypoth	5.79
	408863	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	5.77
20	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	431301	AA602384	Hs.151529	Hs.151529:ESTs	5.71
	418318	U47732	Hs.84072	NM_04616:Homo sapiens transmembrane 4 s	5.71
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	5.68
25	436972	A2A84679	Hs.25640	Hs.25640:cldnln 3	5.66
	414987	AA624394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	5.61
	431657	A1345227	Hs.105448	Hs.105448:protein kinase, lysine deacti	5.67
	424273	W40460	Hs.144442	NM_003581:Homo sapiens phosphopase A2,	5.55
	413816	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.54
30	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.50
	426227	U67058	Hs.154299	{locuslink}NM_005242:Homo sapiens coagut	5.38
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	5.33
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	5.32
35	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.32
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	5.28
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.28
	444151	AW972917	Hs.128749	{locuslink}NM_014324:Homo sapiens alpha-	5.27
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.26
40	408704	AA056635	Hs.5388	NM_139053:Homo sapiens epidermal growth	5.25
	414798	A1286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	5.25
	436251	BE515065	Hs.298685	{locuslink}NM_005392:Homo sapiens nucleo	5.25
	414753	AF158255	Hs.77225	NM_005437:Homo sapiens ADP-ribosyltransf	5.23
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid Ind	5.22
45	443981	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interme	5.20
	432978	AF126743	Hs.279884	NM_019236:Homo sapiens DNAJ domain-conta	5.18
	425834	NM_001639	Hs.1857	Hs.1957:amyloid P component, serum	5.13
	432179	X75208	Hs.28113	NM_004443:Homo sapiens EphB3 (EPHB3), mR	5.12
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	5.11
50	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.08
	426174	AA547959	Hs.115833	Hs.115833:ESTs	5.07
	403218			5.07	
	411142	NM_014253	Hs.69009	NM_014253:Homo sapiens UDP-GlcNAc:betaGa	5.00
55	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.98
	438083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	4.98
	431779	AW871178	Hs.268571	{locuslink}NM_001645:Homo sapiens apolip	4.92
	421408	AI568223	Hs.91095	NM_052816:Homo sapiens tripartite motif-	4.91
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.91
	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.90
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
60	424010	AL080188	Hs.137566	NM_033100:Homo sapiens MT-prolactadherin	4.86
	429953	AA306810	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25-dihydroxyvitami	4.83
	425983	AK000226	Hs.165819	NM_031265:Homo sapiens mucin and cadherin	4.81
65	428289	M26301	Hs.2253	Hs.2253:complement component 2	4.79
	418322	AA2B4166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	4.78
	409689	AW860041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.77
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	423164	AK000232	Hs.124835	NM_019052:Homo sapiens hypothetical prot	4.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MA30	4.72
70	430680	AW138724	Hs.168974	Hs.168974:ESTs	4.69
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidized low dens	4.69
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 f	4.67
	403221			4.65	
	415000	AW025529	Hs.239612	Hs.239612:serologically defined breast c	4.65
75	433437	U20536	Hs.3280	NM_001258:Homo sapiens caspase 6, apopto	4.64
	414062	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	4.64
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.64
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	4.60
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.60
	410639	AW269047	Hs.65234	{locuslink}NM_017895:Homo sapiens DEAD/H	4.60
	411393	AW797437	Hs.59771	NM_001710:Homo sapiens B-factor, properd	4.59
	431193	AW749506	Hs.296770	Hs.296770:KIAA1719 protein	4.57
80	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.56

	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectomucoside tr	4.55
5	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens siatidase 1 (lys	4.54
	431548	AB34273	Hs.9711	NM_071516:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
10	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
	432378	AM493046	Hs.146133	Hs.146133:ESTs	4.48
15	431858	XG3629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
	422511	AL075442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
20	445417	AK001058	Hs.12880	Hs.12880:Homo sapiens cDNA FLJ10196 fs,	4.44
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.43
	428479	Y00272	Hs.334562	NM_001746:Hom sapiens cell division cyc	4.40
25	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23636	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
	439453	BE264974	Hs.6568	Hs.6568:thyroid hormone receptor interac	4.35
30	409231	AA446644	Hs.692	NM_022354:Homo sapiens tumor-associated	4.33
	432575	A553722	Hs.194346	Hs.194346:Spir-2 protein	4.33
	427747	AW411425	Hs.180665	(locuslink)NM_004217:Homo sapiens serine	4.33
	439953	AW247529	Hs.6793	Hs.6793:platelet activating factor acetyl	4.32
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.32
35	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424625	AF207059	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.116274:Indian hedgehog homolog (Dros	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fs	4.29
40	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fs	4.29
	422163	AF027208	Hs.112360	Hs.112360: prominin-like 1 (mouse)	4.28
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fs	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens frosin triphosph	4.27
45	414361	AA086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.22
	420039	NM_004605	Hs.376147	NM_376147:Homo sapiens cDNA FLJ39099 fs	4.20
50	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
	421606	BE302798	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens tylsyl oxidase-lik	4.18
	409142	AL136677	Hs.50768	Hs.50768:SMC4 structural maintenance of	4.18
55	419508	AW997938	Hs.90786	NM_003788:Homo sapiens ATP-binding casse	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncotic receptor inducing	4.17
	408113	TB2427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
	425743	BE395495	Hs.159428	NM_138781:Homo sapiens BCL2-associated X	4.15
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.15
60	453237	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)glycoprota	4.14
	403219				4.14
	407103	AAA24881	Hs.256301	Hs.256301:hypothetical protein MGC19170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
65	409656	AW103364	Hs.727	NM_002192:Homo sapiens fibrin, beta A (4.12
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
	426397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
	413753	U17760	Hs.75517	NM_002228:Homo sapiens fibrin, beta 3 (4.11
	428698	AA852773	Hs.334838	Hs.334838:KAA1866 protein	4.10
70	427557	NM_002659	Hs.179657	NM_02659:Homo sapiens plasminogen activ	4.09
	416123	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
	417866	AW057903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
	426247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.05
75	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
	412812	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.04
	425280	U31519	Hs.1872	NM_022591:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
	452721	AJ269520	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
80	450737	AW007152	Hs.53325	Hs.53325:transmembrane protease, serine	4.01
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78998	NM_002592:Homo sapiens proliferating cell	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphotriboylgly	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antigen	3.97
	414695	BE439915	Hs.76913	Hs.76913:prolesome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
10	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.96
	412133	U63460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	N22768	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
15	400130		Hs.156560	NM_001746:Homo sapiens calnexin (CANX)	3.93
	430696	AA631276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.3805	Hs.9805:exparin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalane epoxidase	3.92
	456529	AW881966	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
20	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
	422293	X94453	Hs.114366	Hs.114366:pyrrolidine-5-carboxylate synth	3.90
	419488	AA316241	Hs.90691	NM_005993:Homo sapiens nucleophosmin/nuc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutase	3.89
	447343	AA255641	Hs.236694	Hs.236694:ESTs, Highly similar to S02392	3.88
25	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AB855116	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens fibromonyl upregu	3.86
30	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	3.85
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020367:Homo sapiens RAB26, member RAS	3.84
	418526	BE019020	Hs.85938	NM_004207:Homo sapiens solute carrier fa	3.84
	426998	AU078629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.84
35	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.83
	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170196	Hs.170195:bone morphogenic protein 7 (3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
40	424441	X14850	Hs.147079	Hs.147079:H2A histone family, member X	3.81
	426378	U80082	Hs.169500	Hs.169500:KIAA0826 protein	3.81
	408636	AA305729	Hs.18272	(locuslink)NM_030574:Homo sapiens solute	3.81
	407786	AA667538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11982	NM_030766:Homo sapiens apoptosis regulat	3.79
	414561	AI064813	Hs.195155	He.195155:solute carrier family 38, memb	3.79
45	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.79
	400529				3.79
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
50	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinet	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.77
	443639	BE289042	Hs.9801	Hs.9801:prolesome (prosome, macropain)	3.76
55	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	3.76
	431350	AI192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cyste	3.75
	435099	AC004770	Hs.4766	NM_004111:Homo sapiens flap structure-sp	3.75
	418216	A4662240	Hs.283099	Hs.283099:AF15q4 protein	3.74
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
60	413063	AL035737	Hs.75184	Hs.75184:citrinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
	444664	N26362	Hs.11616	NM_016086:Homo sapiens map kinase phosph	3.72
65	450334	AF035859	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032632:Homo sapiens hypoth	3.72
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	3.71
70	427333	AF057797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
	434203	BE262677	Hs.283558	NM_018508:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179809	(locuslink)NM_024031:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
	437016	AI076916	Hs.5388	Hs.5398:guanine monophosphate synthetase	3.69
75	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fl	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
	413813	M96958	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
80	431930	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter sl	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte act	3.67

	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.66
5	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	3.66
	413095	AA494369	Hs.30715	Hs.30716:potassium voltage-gated channel	3.66
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	3.64
	404826				3.63
10	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	AI858183		BF755039:QVO-CT0583-181000-42B-07 CT058	3.62
	428072	BE256602	Hs.182366	NM_016292:Homo sapiens heat shock protei	3.61
15	439223	AW238299	Hs.250818	NM_025217:Homo sapiens UL16 binding prot	3.60
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449657	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
20	406684	X16364	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.58
	424534	DB7682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens clspa	3.58
	417526	AA588906	Hs.82240	Hs.82240:syntexin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens glutaminyl phosph	3.57
25	424154	AF026004	Hs.141680	NM_004368:Homo sapiens chloride channel	3.57
	432886	BE158028	Hs.279704	Hs.279704:chromatin accessibility comple	3.56
	413880	AI680842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.55
	421357	AK000609	Hs.103808	NM_017895:Homo sapiens chromosome 20 ope	3.55
	436827	HT2187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.55
30	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidine	3.55
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.55
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	421115	AK001763	Hs.73239	NM_73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_008848:Homo sapiens IMP (inosine mono	3.54
	431512	BE270734	Hs.2795	Hs.2795:deacte dehydrogenase A	3.54
35	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.54
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.53
	414812	X72755	Hs.77367	NM_022418:Homo sapiens macrophage induced	3.53
40	423088	M25629	Hs.123107	NM_02257:Homo sapiens kalikrein 1, ren	3.53
	443160	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.53
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.53
	449057	AB037784	Hs.22941	NM_22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.52
45	412641	M16680	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413761	J05272	Hs.850	(locuslink)NM_008883:Homo sapiens IMP (i	3.51
	409213	U51412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.51
	447200	BE543148	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.51
50	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	3.51
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein tp-regulate	3.51
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alp5, S. cerevis	3.51
	411678	AI907114	Hs.71465	NM_003128:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.51
55	419693	AA133749	Hs.301350	Hs.301350:FXYD domain-containing ion tra	3.51
	407971	AI469117	Hs.52918	Hs.62918:CDC91 cell division cycle 91-II	3.50
	424665	AF011333	Hs.158583	NM_002349:Homo sapiens lymphocyte antige	3.50
	432211	BE274590	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	438014	AF281134	Hs.283741	NM_021658:Homo sapiens exosome component	3.50
60	436278	BE395280	Hs.5097	Hs.5097:synaplogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.50
	428788	AF082283	Hs.183516	NM_003921:Homo sapiens B-cell CLL/lympho	3.50
	424909	S78167	Hs.163752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.49
65	417129	A1381800	Hs.300684	Hs.300684:calcium gene-related peptid	3.49
	409463	A1458185	Hs.17286	NM_023930:Homo sapiens hypothetical prot	3.48
	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ3433 fis	3.48
70	423760	AF165683	Hs.298229	NM_012394:Homo sapiens pretilorin 2 (PFDN	3.47
	446946	AI878932	Hs.317	NM_003288:Homo sapiens topoisomerase (DN	3.47
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	A1272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.45
	407770	AW807831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.45
75	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.86593	NM_019034:Homo sapiens rax homolog gene	3.44
	425209	AL049761	Hs.155140	NM_001695:Homo sapiens caserin kinase 2,	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
80	428023	NM_000312	Hs.2351	NM_00312:Homo sapiens protein C inacti	3.43
	428459	AF151812	Hs.169932	NM_015986:Homo sapiens serologically def	3.43
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mal transforming	3.43
	428093	AW594508	Hs.104830	Hs.104830:ESTs	3.43

	414662	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.43
	400750				3.42
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	3.41
5	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	3.40
	453857	ALB0235	Hs.356651	Hs.356651:Ras-induced senesce 1	3.40
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lk	3.39
	410315	AL638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.39
	428206	AB020643	Hs.183008	Hs.183008:likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.39
	413179	N99592	Hs.75227	NM_00502:Homo sapiens NADH dehydrogenase	3.38
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.38
	400847				3.37
	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	3.37
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	3.37
15	432633	A1796390	Hs.210667	Hs.210667:ESTs	3.36
	429344	R54038	Hs.374664	NM_005638:Homo sapiens Inhibin, beta C (3.36
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.36
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknown	3.35
20	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGL-06 protein (L	3.35
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.35
	400848				3.35
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.35
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small Inducible c	3.35
25	418412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.35
	428284	AA256363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.34
	425322	U63830	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.34
30	46291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.34
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.34
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.34
35	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.33
	439976	AI118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.33
	418418	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cr+-tran	3.33
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens Similar to LOC16	3.33
40	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.33
	432320	AW411068	Hs.274351	NM_018032:Homo sapiens zinc finger, DHHC	3.33
	444019	BE173877	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278513	(locuslink)NM_005532:Homo sapiens Interf	3.32
	410219	T98228	Hs.171952	Hs.171952:occludin	3.32
45	410563	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.32
	402828				3.32
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.32
	414198	AW505308	Hs.75812	NM_044583:Homo sapiens phosphoenolpyruva	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
50	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.31
	410288	AA316181	Hs.81635	NM_012449:Homo sapiens six transmembrane	3.30
	425159	NM_004341	Hs.164868	NM_004341:Homo sapiens carboxyl-phospho	3.30
	420614	AL110291	Hs.99364	Hs.99364:carboxylesterase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247:Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033:Homo sapiens rbohucleotide re	3.30
	409402	AF208234	Hs.695	Hs.695:cystatins B (stefin B)	3.30
	421038	AI080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.29
	424403	A1754813	Hs.145428	Hs.145428:collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_02452:Homo sapiens nudix (nucleoside	3.29
60	442821	BE391829	Hs.8752	Hs.8752:transmembrane protein 4	3.29
	459305	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422256	M64573	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.28
	408089	H59799	Hs.42644	Hs.42644:flavodoxin-like 2	3.28
65	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.27
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_136569:Homo sapiens protein phosphata	3.27
	447335	BE817695	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.27
	414388	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.27
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic 1, protein	3.26
70	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22959	3.26
	431183	NM_008555	Hs.250698	NM_008555:Homo sapiens KDEL (Lys-Asp-Glu	3.26
	457635	AV660978	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.26
	432391	A1732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.26
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.25
75	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-tal simila leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.25
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens aducin	3.25
	407236	WT9485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.25
	447250	AB786909	Hs.17883	NM_0027073:Homo sapiens protein phosphata	3.25
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.24
	428390	A1640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.24
	426811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.24

	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contal	3.24
5	419170	BE002798	Hs.287850	NM_002219:Homo sapiens Integral membrane	3.24
	428858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE288623	Hs.149155	(locuslink)NM_003374:Homo sapiens voltage	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitofic arrest deficient-1	3.23
10	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.23
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinase	3.23
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
	420185	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	3.22
15	448153	Y10805	Hs.20521	NM_001636:Homo sapiens HMT1 hnRNP methyl	3.22
	425274	BE281191	Hs.155462	Hs.155462;MCM6 minichromosome maintenanc	3.21
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	AT741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
20	421006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630068	Hs.76560	NM_052886:Homo sapiens maf, T-cell diffe	3.20
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
25	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transmembrane protein 1, AT	3.20
	413431	AW248428	Hs.75355	NM_003348:Homo sapiens ubiqutin-conjugat	3.19
	437379	AL358575	Hs.23785	Hs.23785:membrane metallo-endopeptidase	3.19
	408716	AI567838	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
30	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfact 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripe	3.19
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutal	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens Interleukin 2 rec	3.18
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.18
	445580	AF167572	Hs.12912	NM_008109:Homo sapiens SKB1 homolog (S.	3.18
35	420531	AI852069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
	417389	BE260964	Hs.82045	Hs.82045:mildlndn (neurite growth-promot	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.18
	414883	AA926960	Hs.348669	Hs.348669:CD28 protein kinase 1	3.18
	421743	T35958	Hs.107614	Hs.107614:DKFZP56411171 protein	3.18
	447698	AI420165	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL038662	Hs.144949	Hs.144949:ESTs	3.17
45	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC24)	3.17
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
	449944	AF290312	Hs.58215	(locuslink)NM_033046:Homo sapiens rhoek	3.17
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
50	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
	447151	AI022813	Hs.92679	(locuslink)NM_14754:Homo sapiens kinase	3.15
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
	410836	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
55	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens parox	3.15
	435885	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
	458778	AW451034	Hs.328525	NM_001689:Homo sapiens arylsulfatase D (3.14
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428271	AI012193	Hs.183874	NM_035699:Homo sapiens culin 4A (CUL4A)	3.14
60	450580	AA295698	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYD d	3.14
	413900	AW409747	Hs.75612	NM_006319:Homo sapiens stress-induced-ph	3.13
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:aridine kinase-like 1	3.13
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
65	426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE3B5750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
	420675	AI434780	Hs.42428	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	AI056470	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE3458	3.12
	439778	AI109729	Hs.89364	Hs.99364:abhydrolase domain containing 1	3.12
	412328	RO7556	Hs.73817	NM_022983:Homo sapiens small inducible c	3.12
	447556	NM_003726	Hs.19126	NM_003726:Homo sapiens ec family associ	3.12
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	AI879159	Hs.108219	NM_004528:Homo sapiens wingless-type MMT	3.11
	400262		Hs.75309	NM_001951:Homo sapiens eukaryotic transl	3.11
70	418803	U50079	Hs.88566	NM_004964:Homo sapiens histone deacetylase	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AAS24545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33348 fis	3.11
	433179	AW362945	Hs.182459	Hs.162459:ESTs	3.11
	452264	AI077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
75	418841	BE243135	Hs.86947	NM_001108:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.108196	(locuslink)NM_016570:Homo sapiens B26 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Fink1	3.10
	457670	AF119566	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

	438407	AI457122	Hs.128673	Hs.129873:eukaryotic translation Initia	3.10
	428293	BE260944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.10
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 284	3.10
5	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22285	Hs.22285:pyruvate dehydrogenase phosphat	3.10
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.09
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
	404240				3.08
10	408989	AW361666	Hs.49500	Hs.49500:Q3AA0746 prot	3.08
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	448506	AI123118	Hs.15159	[locuslink]NM_016326:Homo sapiens chemok	3.08
	402260				3.08
15	428711	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
	445937	AI452943	Hs.321231	[locuslink]NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_022959:Homo sapiens syndecan 4 [amph	3.07
	422611	AA158177	Hs.118722	[locuslink]NM_004480:Homo sapiens fucosy	3.07
20	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.07
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	454128	AL031259	Hs.357900	Hs.357900:programmed cell death 2	3.07
25	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.07
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
	428640	BE382756	Hs.169902	NM_0065163:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
30	435750	AB029012	Hs.4990	Hs.4980:KIAA1069 protein	3.06
	421802	BE261458	Hs.108408	[locuslink]NM_016022:Homo sapiens CGI-78	3.06
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens. Similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427288	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
35	412525	AA581439	Hs.152328	[locuslink]ESTs	3.06
	422B13	AV658571	Hs.121068	[locuslink]NM_003270:Homo sapiens transm	3.05
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408805	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4884	Hs.4984:KIAA0828 protein	3.05
40	432871	NM_016142	Hs.279517	Hs.279517:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005091:Homo sapiens NADH dehydrogenas	3.05
	425268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
45	406363				3.05
	439841	AF038961	Hs.5710	NM_004870:Homo sapiens mannoe-P-dolicho	3.05
	431730	AW237728	Hs.288549	NM_028228:Homo sapiens ubiquitin UbF-II	3.04
	447966	AA340605	Hs.105887	[locuslink]NM_145252:Homo sapiens simila	3.04
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
50	427597	D15049	Hs.179770	NM_028442:Homo sapiens protein tyrosine	3.04
	430281	AI678842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AI128808	Hs.179902	[locuslink]NM_022109:Homo sapiens Cd69	3.04
	452885	AB24046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	3.04
55	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.04
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR das	3.04
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.03
	417777	AI822763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ3420 fis,	3.03
	417144	A3382104	Hs.81337	Hs.81337:ectein, glycoside-binding, so	3.03
60	450825	AC005954	Hs.25527	[locuslink]NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plaminogen activ	3.03
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE-3881	3.03
	440659	AF134160	Hs.7527	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	422268	BE311856	Hs.274220	Hs.274220:3'-phosphoadenosine 5'-phospho	3.03
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.02
65	412659	AU076782	Hs.246257	[locuslink]NM_021126:Homo sapiens mercap	3.02
	420788	U66515	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	425966	NM_001781	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI507180	Hs.110306	Hs.110906:hypothetical protein BC004501	3.02
	431236	AV656840	Hs.285115	NM_015682:Homo sapiens Interferon 13 re	3.02
70	414702	L22005	Hs.76832	NM_004359:Homo sapiens cell division cyc	3.02
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018882	Hs.166195	Hs.166195:ATPase, Class I, type 8B, memb	3.01
	437712	X04588	Hs.85844	Hs.85844:neurotrophin tyrosine kinase, r	3.01
75	410283	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.01
	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.00
	447032	AK000310	Hs.17138	[locuslink]NM_017755:Homo sapiens hypoth	3.00
	414249	A179944	Hs.279929	NM_017610:Homo sapiens gp251.2	3.00
80	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 firs	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE-29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
5	412148	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
	437763	AA469369	Hs.5831	Hs.5831:inhibitor of metalloprotease	2.99
	408665	AI026931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	2.99
	425725	NM_012243	Hs.159322	(focuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
10	432396	AW295956	Hs.11900	(focuslink)NM_032527:Homo sapiens hypoth	2.98
	411358	R47479	Hs.84761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 firs	2.98
	440913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6)	2.98
15	440943	AW082298	Hs.146161	NM_022331:Homo sapiens hypothetical prot	2.98
	414013	AA766605	Hs.47089	NM_024642:Homo sapiens hypothetical prot	2.98
	462124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	A1678927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89803	NM_002456:Homo sapiens muclin 1, transmem	2.97
20	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437298	AA350994	Hs.20281	HS.20281:MAPK phosphatase-7	2.97
	407736	N41744	Hs.349328	Hs.349328:Homo sapiens cDNA FLJ30877 firs	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(focuslink)NM_002295:Homo sapiens lamin	2.97
25	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(focuslink)NM_000577:Homo sapiens interl	2.97
	425271	AV849864	Hs.155188	NM_006642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostasin)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
30	452012	AA307703	Hs.279766	(focuslink)NM_012310:Homo sapiens kinesin	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW966941	Hs.168254	Hs.168254:likely ortholog of rat vacuole	2.96
35	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
	445360	AF052112	Hs.12540	NM_008330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(focuslink)NM_145059:Homo sapiens L-fuco	2.96
	429597	NM_003816	Hs.2442	Hs.2442:alpha disintegrin and metalloprotein	2.95
	421179	U72684	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
40	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430588	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	2.95
	409220	BE243323	Hs.51233	(focuslink)NM_003842:Homo sapiens tumor	2.95
	443883	AA114212,	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
45	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
	429583	NM_008412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.178703	NM_014788:Homo sapiens tripartite motif-	2.94
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyldiphosph	2.94
50	419152	L12711	Hs.89643	(focuslink)NM_001064:Homo sapiens transk	2.94
	444824	AA843575	Hs.12058	NM_001671:Homo sapiens astroglycoprotein	2.94
	431829	AU0777025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU078611	Hs.154672	Hs.164672:ethylene tetrahydrofuran dalt	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ32230 firs	2.93
55	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA161527	Hs.69485	(focuslink)NM_024861:Homo sapiens hypoth	2.93
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AA899496	Hs.108932	Hs.108932:ESTs	2.93
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
60	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens sphm-B1 (EFNB1)	2.92
	417544	AU077196	Hs.82895	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(focuslink)NM_145294:Homo sapiens simila	2.92
	439640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
65	451608	AA384525	Hs.26745	NM_016499:Homo sapiens H8PC244 (MGC:1337	2.92
	434608	AA806443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
	437166	AA336308	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 firs	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
70	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 firs	2.91
	444193	Y17B01	Hs.10574	Hs.10574:solute carrier family 2, (faci	2.91
	422030	X51416	Hs.110849	(focuslink)NM_004451:Homo sapiens estrogen	2.91
	415938	BE383607	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
	430167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
75	408815	AW957974	Hs.26485	(focuslink)NM_024598:Homo sapiens hypoth	2.91
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colicin	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262988	Hs.12046	Hs.12045:C21 protein	2.91
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
80	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	2.90
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.90
	412926	A1879076	Hs.75061	Hs.75061:macrophage myristoylated alanyl	2.90

	455967	L12535	Hs.75551	(locuslink)NM_012425:Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens fernes	2.90
5	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cytoso	2.90
	456157	AW979153	Hs.336881	Hs.336881:ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274:Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	NM_003028:cDNA FLJ3890B fis	2.89
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	2.89
10	438543	A8A10141	Hs.192182	Hs.192182:ESTs	2.89
	426168	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.89
	441456	AJ271671	Hs.7854	NM_014437:Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797:Homo sapiens proteasome (proso	2.89
15	409591	AA532953	Hs.9100	Hs.9100:hypothetical gene supported by A	2.89
	418062	AW830656	Hs.83393	NM_006406:Homo sapiens peroxidoxin 4 (2.89
	436540	BE397032	Hs.14488	NM_020230:Homo sapiens peter pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80867	Hs.80867:v-yes-1 Yamaguchi sarcoma viral	2.89
20	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	2.88
	428404	NM_005738	Hs.10708	NM_005738:Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346:Homo sapiens opioid	2.88
	413622	R08950	Hs.272044	Hs.272044:ESTs, Weakly similar to hypoth	2.88
	438085	RS2518	Hs.7987	Hs.7967:ESTs, Weakly similar to extensin	2.88
25	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	2.88
	440490	AW513684	Hs.7218	Hs.7218:acetyl-Coenzyme A synthetase 2 (2.87
	431498	AK001777	Hs.256551	NM_012100:Homo sapiens aspartyl aminopept	2.87
	423570	AW838306	Hs.129B19	NM_018344:Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	2.87
30	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	2.87
	442643	U82758	Hs.374973	(locuslink)NM_004697:Homo sapiens PRPF4 p	2.87
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419:zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	2.87
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactos	2.87
35	453145	R63438	Hs.183464	Hs.183454:Homo sapiens cDNA FLJ14833 fis	2.86
	427775	R28944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D8D001	Hs.152629	Hs.152629:KIAA0179 protein	2.86
	426125	X87241	Hs.168994	Hs.168994:FAT tumor suppressor homolog 1	2.86
40	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	2.85
	407082	Z47056			2.86
	450038	AA005159	Hs.188489	Hs.188489:ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.85
	417631	H16423	Hs.82585	Hs.82585:CD47 antigen (Rh-related anti ge	2.85
45	417824	A0A084798	Hs.82846	NM_006145:Homo sapiens Dnaj (Hsp40) homo	2.85
	426989	AB162026	Hs.100293	NM_100293:O-linked N-acetylglucosamine (2.85
	434916	AF161383	Hs.284207	Hs.284207:hypothetical protein BC0036515	2.85
	412664	AA421404	Hs.346868	NM_006244:Homo sapiens EBNA1 binding pro	2.85
	414172	AW554324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	2.85
	409504	AA304961	Hs.699	Hs.699:peptidyl prolyl isomerase B (cyclo	2.84
50	439920	H05430	Hs.288433	NM_016522:Homo sapiens neurothrin (HNT)	2.84
	418462	BE001586	Hs.85266	NM_008266:integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879:Homo sapiens capping-stimulus-induced	2.84
	405710	AI708347	Hs.184014	Hs.184014:ribosomal protein L31	2.84
55	433435	BE645277	Hs.340959	NM_005726:Homo sapiens Ts translation el	2.84
	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	2.84
	448730	AB002983	Hs.21894	Hs.21894:KIAA1157 protein	2.84
	433027	AF191018	Hs.279323	(locuslink)NM_014366:Homo sapiens putat	2.84
	449090	AK001735	Hs.22983	NM_020121:Homo sapiens UDP-glucose caram	2.84
60	439737	AT751438	Hs.41271	Hs.41271:Homo sapiens mRNA full length i	2.84
	403912				2.84
	423225	AA852604	Hs.125358	NM_006288:Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059:KIAA0982 protein	2.84
	429211	AF052683	Hs.198249	NM_005268:Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24758	Hs.24758:Homo sapiens cDNA FLJ32068 fis,	2.84
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	2.83
	448489	AI523875		R45782:Hsa6164:f adult heart, Clotech Hom	2.83
	426194	T50872	Hs.2001	NM_001061:Homo sapiens thrombokane A syn	2.83
	421219	AI076635	Hs.1478	NM_000185:Homo sapiens serine (or cyste	2.83
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	2.83
	423323	AB51628	Hs.127007	NM_003740:Homo sapiens potassium channel	2.83
	439720	AI935202	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.83
75	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155965	Hs.155965:ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	2.82
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.82
80	415597	AB365603	Hs.279698	Hs.279698:DUFZP56611024 protein	2.82
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of esr	2.82
	430040	AW503115	Hs.227823	NM_014267:Homo sapiens pM5 protein (PM5)	2.82
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AJ167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fts	2.82
	400845				2.81
5	419501	AW843822	Hs.189961	Hs.189961:ESTs, Weekly similar to hypoth	2.81
	418140	BE513536	Hs.83551	(focuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476968	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_002280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(focuslink)NM_005886:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433051	AW068033	Hs.298422	(focuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fts,	2.81
	410240	AL157424	Hs.51289	Hs.61209:synaptosomal 2	2.80
	423680	BE278111	Hs.134200	Hs.134200:DKFZP584C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:Homo sapiens tRNA	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456602	AA411607	Hs.116954	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(focuslink)NM_016442:Homo sapiens type I	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74275	Hs.74276:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003868:Homo sapiens nitrogen-activated	2.79
	409531	BE384319	Hs.54702	(focuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419848	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren a	2.79
30	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005767:Homo sapiens Not56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fts	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(focuslink)NM_005723:Homo sapiens tetras	2.79
35	449762	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
	419236	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrophin (NNT)	2.78
	407754	AA527348	Hs.288967	Hs.288967:Homo sapiens, similar to RIKEN	2.78
	422262	AF018225	Hs.114309	(focuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418860	AW516556		AA229762nc49101r1 NCL_CGAP_Pr3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016029	Hs.283021	NM_016928:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54620	Hs.351327	(focuslink)NM_017828:Homo sapiens hypoth	2.78
45	417895	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(focuslink)NM_005964:Homo sapiens solute	2.78
	450507	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
	419757	AA77320	Hs.63970	Hs.63970:ESTs	2.77
50	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206039	Hs.42287	NM_001852:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(focuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	445950	AA305800	Hs.5572	(focuslink)NM_030799:Homo sapiens golgi	2.77
	442407	AI665004	Hs.374416	Hs.374416:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fts	2.77
	445985	BE521800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE263927	Hs.24963	Hs.24983:hypothetical protein from EURO	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333525	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12260 fts	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
65	450770	AA019324	Hs.28803	Hs.28803:ESTs	2.76
	419584	AA013051	Hs.91417	(focuslink)NM_007027:Homo sapiens topois	2.76
	450876	AF189062	Hs.285976	(focuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417757	BE242241	Hs.82542	NM_001637:Homo sapiens acylxoyacyl hydro	2.76
	439988	AA224760	Hs.153	NM_00971:Homo sapiens ribosomal protein	2.76
70	426520	BE545564	Hs.343566	Hs.343566:tRNAAsp1 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	NM_078467:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
	428157	AT738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
75	416178	AI806527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435026	T08990	Hs.4742	Hs.4742:GPAA1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57908	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
	408196	AL034548	Hs.43627	NM_008943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
80	421643	BE281170	Hs.105357	NM_007126:Homo sapiens valosin-containin	2.74

	423627	AI208965	Hs.105861	(focuslink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PI/GPC1	2.74
5	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	2.74
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens vblquintol cytochr	2.74
	440457	BE387593	Hs.21321	(focuslink)NM_145808:Homo sapiens granul	2.74
	422675	BE016517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037644	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
10	423598	BE247800	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cyste)	2.73
	421921	H383363	Hs.365993	NM_012455:Homo sapiens translocase of in	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to chot	2.73
15	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synth	2.73
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
20	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
	436895	AI160015	Hs.125489	Hs.125489:KAIA1981 protein	2.73
	400509				2.73
25	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
	446899	AI263738	Hs.145628	Hs.145628:Homo sapiens, Similar to hypot	2.72
	453557	AA622464	Hs.285995	NM_024956:Homo sapiens hypothetical prot	2.72
	446859	AI494299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579535	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5865	Hs.5865:Homo sapiens mRNA; cDNA DKFZp434	2.72
30	428466	AF151063	Hs.184456	NM_010486:Homo sapiens hypothetical prot	2.71
	445176	AI978907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	2.71
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector prot	2.71
	429359	W00462	Hs.2399	NM_004995:Homo sapiens matrin metaloprote	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H ⁺ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
	426263	A1908774	Hs.259785	Hs.259785:carnitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416876	BE243985	Hs.80860	Hs.80860:major vault protein	2.71
40	441238	AI372655	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
	424965	AW956282	Hs.1446509	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
	410113	AW996564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 f	2.70
45	413092	AA126B56	Hs.118665	Hs.118665:ESTs	2.70
	447098	BE539199	Hs.62112	(focuslink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
	413745	AW247262	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
50	436042	AF284422	Hs.119178	(focuslink)NM_020246:Homo sapiens caton	2.70
	432981	NM_002733	Hs.3135	Hs.3135:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43668	NM_007079:Homo sapiens protein tyrosine	2.70
	416720	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H56698	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
	424500	AF040704	Hs.149443	(focuslink)NM_007022:Homo sapiens putati	2.69
	414237	BE536554	Hs.278270	Hs.278270:unactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
60	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04,s1 NCL_CGAP_Pt2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
	449857	D31365	Hs.24220	(focuslink)NM_016478:Homo sapiens sctin	2.69
65	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA	2.69
	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005097:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BEN-E protein	2.68
	446139	AB037840	Hs.12365	Hs.12365:cyneaptidegranin XII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD/H (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntaxin 4A (plec	2.68
	409533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
70	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of cu	2.68
	455303	AW892049		BE066891:PM3-BT0338-21239-002-e12 BT033	2.68
	452600	AI910B42	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paroxonase 2 (PO	2.67
	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 protein {	2.67
	433339	AF019226	Hs.8336	NM_004283:Homo sapiens RAB3D, member RAS	2.67
75	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67	
427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67	
436318	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67	
5	415116	AA160363	Hs.259956:ESTs	2.67	
425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66	
418706	U73524	Hs.87465	NM_005831:Homo sapiens ATP/GTP-binding p	2.66	
410165	BE580228	Hs.71869	NM_013258:Homo sapiens apoptosis-associa	2.66	
410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66	
10	430066	A1929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
426910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66	
427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxin 1 (MTX1),	2.66	
439871	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fs	2.66	
438449	AK001333	Hs.6216	Hs.6216:Dnaj (Hsp40) homolog, subfamily	2.66	
15	435906	A1686379	Hs.110798	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
433387	L76528	Hs.3250	NM_000221:Homo sapiens presenilin 1 (Alz	2.66	
447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66	
444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66	
417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66	
20	418529	AW005695	Hs.250897	Hs.250897:TRK-fused gene	2.66
426025	AW136330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE-40704	2.65	
420187	AK001714	Hs.95744	NM_018028:Homo sapiens hypothetical prot	2.65	
408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65	
444396	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65	
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zonapellucida gl	2.65
405790	AA293303	Hs.355342	Hs.355342:ESTs, Highly similar to 211320	2.65	
440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65	
418526	H61082	Hs.14743	Hs.14743:ESTs	2.65	
413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (sxt)	2.65	
30	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
442110	AF113008	Hs.81102	NM_001023:Homo sapiens ribosomal protein	2.65	
452882	AW972890	Hs.195270	NM_030780:Homo sapiens folate transpote	2.65	
406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64	
451295	A557212	Hs.17132	Hs.17132:ESTs	2.64	
35	448428	AE282874	Hs.21201	NM_015402:Homo sapiens neclin 3 (DKFZP56	2.64
426611	BE178050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64	
426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fs,	2.64	
407223	H96850		H96850:yw03b12.s1 Soares melanocyte 2NbH	2.64	
427725	U66839	Hs.180533	NM_002755:Homo sapiens mitogen-activated	2.64	
420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64	
40	428471	X57348	Hs.184510	Hs.184510:stratifin	2.64
451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64	
413245	BE2444334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64	
415020	BE249915	Hs.299533	Hs.299533:Homo sapiens cDNA FLJ37093 fs	2.64	
437193	BE250190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64	
45	418664	UB2987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
410568	BE379794	Hs.159851	NM_014452:Homo sapiens tumor necrosis fa	2.64	
438183	A146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64	
441226	BE563042	Hs.118820	Hs.118820:hypothetical protein BC070862	2.64	
50	432768	AA521091	Hs.178499	Hs.178499:HSPC083 protein	2.64
432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64	
450377	AB033091	Hs.355925	Hs.355925:KIAA1285 protein	2.64	
434653	A189587	Hs.120915	Hs.120915:ESTs	2.64	
424707	BE031914	Hs.10844	Hs.10844:sugue-rich alpha-2-glycoprote	2.64	
55	427600	AW630918	Hs.179774:proteasome (prosome, macropain	2.63	
446522	NM_003876	Hs.15198	NM_003876:Homo sapiens putative receptor	2.63	
436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	2.63	
410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63	
410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63	
60	408716	AW148846	Hs.169476:glyceraldehyde-3-phosphate deh	2.63	
430308	BE540865	Hs.238990	NM_004084:Homo sapiens cyclin-dependent	2.63	
431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63	
412867	AI076881	Hs.74637	Hs.74637:tes1 enhanced gene transcript	2.63	
440524	R71254	Hs.15798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63	
65	435658	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	2.63
422872	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63	
447528	A612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63	
406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63	
439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63	
70	435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
428589	AW578252	Hs.190181	Hs.190181:LRR protein	2.62	
410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fs	2.62	
414839	X63692	Hs.77462	(locuslink)NM_001378:Homo sapiens DNA (c	2.62	
443217	NM_001645	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62	
448749	AW859879	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62	
75	450009	AI39947	Hs.166485	Hs.166485:Homo sapiens cDNA FLJ11432 fs	2.62
407667	AK002011	Hs.37558	NM_016339:Homo sapiens hypothetical prot	2.62	
442232	A1357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62	
419626	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62	
416114	A1695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62	
80	439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal)	2.61
408452	AA054983	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fs	2.61	
443142	A1696513	Hs.108705	Hs.108705:protein phosphatase 2 (former	2.61	
426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61	

	419667	AU077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
	403399				2.61
5	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW031061	Hs.103180	Hs.103180:DC2 protein	2.61
10	446488	AB037782	Hs.15119	Hs.15119:KIAA1361 protein	2.61
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AJ475124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	{focuslink}NM_012280:Homo sapiens FtsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
15	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	{focuslink}NM_004069:Homo sapiens adapto	2.60
	450858	C18458	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
20	430504	H52761	Hs.44095	Hs.44095:cyclin M3	2.59
	439578	AW283124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	{focuslink}NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521:Homo sapiens general transcript	2.59
25	422140	BE285918	Hs.112193	{focuslink}NM_025259:Homo sapiens chromo	2.59
	452817	AA322659	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW293542	Hs.75309	Hs.75309:eukaryotic translation elongat	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
30	440511	AF132659	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
	407887	AA579668	Hs.41072	{focuslink}NM_004568:Homo sapiens serine	2.59
	425356	BE244879	Hs.165939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.621	Hs.821:lectin, galactoside-binding, solu	2.59
	417952	A1192638	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
35	433053	BE301909	Hs.279852	NM_015917:Homo sapiens glutathione S-tr	2.59
	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	{focuslink}NM_021959:Homo sapiens prote	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA605112	Hs.282990	NM_003550:Homo sapiens chromosome 20 ope	2.58
40	448438	AV651680	Hs.208558	Hs.208558:ESTs	2.58
	416435	AI31301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:elute carrier family 20 (phosp	2.58
	452222	AW808287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
45	444309	UB3236	Hs.10803	Hs.10803:calcium and integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418523	BE247560	Hs.86859	{focuslink}NM_005310:Homo sapiens growth	2.58
	432995	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
50	426781	AL048967	Hs.172207	{focuslink}NM_007363:Homo sapiens non-PO	2.57
	452636	BE515074	Hs.145279	Hs.145279:SET translocase (myeloid leu	2.57
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447874	BE270640	Hs.19182	NM_001798:Homo sapiens cyclin-dependent	2.57
	445847	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
55	402861				2.57
	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414028	BE287731	Hs.76709	NM_002355:Homo sapiens mannose-6-phosph	2.57
	427700	AA262294	Hs.180583	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW285634	Hs.133109	Hs.133100:ESTs	2.56
60	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 6	2.56
	442599	AF078037	Hs.324051	{focuslink}NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA083322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
	451664	AI076698	Hs.132760	{focuslink}NM_001487:Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	{focuslink}NM_145169:Homo sapiens simila	2.56
	438630	AA313607	Hs.56533	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.56
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyri	2.55
	448279	BE250564	Hs.283555	Hs.283555:dysphosphopholipase II	2.55
70	453360	A1917771	Hs.61790	{focuslink}NM_024650:Homo sapiens Import	2.55
	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205738	Hs.205738:KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	{focuslink}NM_017806:Homo sapiens hypoth	2.55
	449089	D78850	Hs.250465	Hs.250465:Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S.	2.55
	437469	AW753112	Hs.16514	Hs.15514:hypothetical protein MCC3260	2.55
	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis,	2.55
	446673	NM_016361	Hs.15871	NM_016361:Homo sapiens LPAP for lysophos	2.55
	411766	AA399571	Hs.71989	Hs.71969:Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
80	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC:31984	2.55

417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450, (locuslink)NM_021622:Homo sapiens plecks	2.55
443358	H65417	Hs.17757	Hs.29189:ATPase, Class VI, type 11A	2.55
452349	AB028944	Hs.29189	NM_003053:Homo sapiens RAD23 homolog A (2.54
5	427721	A15B2843	Hs.180455 Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
407559	AA313352	Hs.280858	Hs.75354:GCN1 general control of amino-a	2.54
413426	U88837	Hs.75354	Hs.1904:protein kinase C, iota	2.54
425465	L18954	Hs.1904	Hs.149305:hypothetical protein MGC2603	2.54
444152	A1125594	Hs.149305	(locuslink)NM_004556:Homo sapiens nuclea	2.54
10	451820	AW058357	Hs.199248 NM_000958:Homo sapiens prostaglandin E r	2.54
441356	BE384361	Hs.182285	(locuslink)NM_004556:Homo sapiens nuclea	2.54
444410	BE387360	Hs.33719	L033719:Homo sapiens, similar to data s	2.54
415200	ALD040328	Hs.78202	NM_003072:Homo sapiens SW/SNF related,	2.54
	403955			2.54
15	430361	AI033955	Hs.239926:sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
	446719	W39500	Hs.301872:hypothetical protein MGC4840	2.54
	439941	AB392840	Hs.16272 NM_030574:Homo sapiens solute carrier fa	2.54
20	436685	W28661	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AI134847	Hs.149957:ribosomal protein S8 kinase, 9	2.54
	442804	AW576008	Hs.11356 Hs.11355:thymopoietin	2.54
	422605	H16646	Hs.118666:hypothetical protein PP591	2.54
	442069	AW654144	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.54
	447362	AW176120	Hs.9061 NM_024098:Homo sapiens hypothetical prot	2.53
25	416305	AU076628	Hs.79187 NM_001339:Homo sapiens coxsackievirus a	2.53
	422624	BE618678	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
	447298	BE617527	NM_006219:Homo sapiens phosphoinositide-	2.53
	412833	AW960547	Hs.298262:ribosomal protein S19	2.53
	404654			2.53
30	415761	AA132656	Hs.78802 (locuslink)NM_002093:Homo sapiens glycog	2.53
	431104	AW970859	Hs.313503:ESTs	2.53
	439180	A1393742	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	NM_003749:Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
35	415742	BE410243	Hs.78769 NM_003249:Homo sapiens thimet oligopepti	2.53
	404140			2.53
	407255	AA012992	Hs.256301:hypothetical protein MGC13170	2.53
	422609	AA258513	Hs.117865 Hs.117865:solute carrier family 17 (anion	2.63
40	434866	AW002565	Hs.355460:Homo sapiens cDNA: FLJ21763 f	2.63
	429743	AA804398	(locuslink)NM_017951:Homo sapiens hypoth	2.53
	433047	MB6135	NM_004990:Homo sapiens methionine-tRNA s	2.53
	418945	BE246762	Hs.89499:arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826 NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784:prolactin regulatory element b	2.52
45	448252	BE622791	NM_030577:Homo sapiens hypothetical prot	2.52
	447365	BE383676	Hs.334 (locuslink)NM_005435:Homo sapiens Rho gu	2.52
	414844	AA296874	Hs.77494 NM_003916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093 NM_015945:Homo sapiens ovarian cancer ev	2.62
	416149	AA311965	Hs.79058 NM_003168:Homo sapiens suppressor of Ty	2.52
50	418741	HS32625	Hs.8881 Hs.8881:Homo sapiens cDNA FLJ32163 fis,	2.52
	437952	D63209	NM_014585:Homo sapiens solute carrier fa	2.52
	445825	BE246743	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431565	AF161470	Hs.280822:2-butyrate-induced transcript 1	2.52
	410179	W27723	(locuslink)NM_003718:Homo sapiens cell d	2.52
55	431476	SE612705	Hs.256697 (locuslink)NM_006340:Homo sapiens histid	2.52
	406672	M26041	Hs.198253 NM_002122:Homo sapiens major	2.52
	418180	BE618087	Hs.83724:hypothetical protein MGC5468	2.62
	428248	AH128772	Hs.40479:Homo sapiens cDNA FLJ26502 fis,	2.52
	419935	AB020980	Hs.93832:putative membrane protein	2.52
60	446143	BE245342	Hs.308079 NM_013336:Homo sapiens protein transport	2.52
	426691	NM_008201	Hs.171834 (locuslink)NM_006201:Homo sapiens PCTAIR	2.51
	408124	U89337	Hs.42853 NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726 NM_003651:Homo sapiens cold shock domain	2.51
	426921	Z43809	Hs.194638:polymerase (RNA) II (DNA direc	2.51
65	414721	X90392	Hs.77091 NM_006730:Homo sapiens deoxyribonuclease	2.51
	422607	Z45471	Hs.118884 NM_005923:Homo sapiens stromal cell-deri	2.51
	421846	AA017707	Hs.1432 NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515 NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861 NM_015955:Homo sapiens CCL-31 protein [L	2.51
	432893	AA351815	Hs.50740:Homo sapiens mRNA; cDNA DKFZp78	2.51
70	418360	AW296974	Hs.84264 NM_006401:Homo sapiens acidic leucine-r	2.50
	401061			2.50
	426559	AB001914	Hs.170414:paired basic amino acid cleav	2.50
	412204	AI125507	Hs.24937:transformer-2 alpha (fra-2 alp	2.50
75	448950	AF288687	Hs.9275 NM_020410:Homo sapiens CGI-152 protein (2.50
	409836	AK001681	Hs.57655 (locuslink)NM_018234:Homo sapiens chd1l	2.50
	414676	F79015	Hs.288968:RAB22A, member RAS oncogene fa	2.60
	409983	D50922	Hs.57729 (locuslink)NM_012289:Homo sapiens Kelch-	2.50
	450914	A1743761	Hs.142528:Hs.142526:ESTs	2.50
	446630	A1753230	(locuslink)NM_032121:Homo sapiens hypoth	2.50
80	401353			2.50
	441680	AW444598	Hs.7940 (locuslink)NM_021158:Homo sapiens RAP1,	2.50
	406880	AA876469	AA876469;oe48b0;as1 NCI_CGAP_Pr25 Homo s	2.50
	449163	AW161356	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimaerin (chimaerin) 2	2.50
430600	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10603	2.50

5

TABLE 9B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

10

Pkey	CAT Number	Accession
406685	0_0	M18728
452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 A1856183
451129	1495511_1	BE072281 A1762161 BE072946
459306	223120_4	AW578452
448489	2189115_1	R45782 R45781
418869	12769_14	AA229762 AA230035
418546	242836_1	T59708 AA224827 T59843 BE156903
455303	1152492_1	BE088891 BE066895 AW892049 BE068897 BE903884
20	406660	0_0 AA876469

TABLE 9C

25

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., *Nature* (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

30

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
403220	7630969	Plus	84338-64517
403218	7630969	Plus	58039-58149
403221	7630969	Plus	66294-66438,66936-67124
403219	7630969	Plus	61858-81995
403739	7630882	Plus	44563-44766,46209-48483,52255-52495
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
405556	1552511	Plus	163497-163623,164715-164958,165369-16550
406529	9796988	Plus	136232-138423
404826	6572184	Plus	47726-48046
400750	8119067	Plus	198991-199168,199316-199548
400847	9188605	Plus	44643-44835
400448	9887687	Minus	177372-177674
402829	8918414	Plus	101532-101852,102006-102263
400846	9188605	Plus	39310-39474
401179	9439647	Plus	113477-113883
404240	5002624	Minus	116132-116407,116853-116922
402260	3399865	Minus	113765-113910,116853-115765,116808-11694
50	406363	9256114	Plus
	405203	7230116	Plus
	402104	8119072	Plus
	403912	7710730	Minus
	400845	9188605	Plus
	403217	7630969	Plus
	403483	9956188	Minus
	400509	9796539	Minus
	403399	6584178	Plus
	400541	7574902	Plus
	402861	2814366	Minus
	403955	7770475	Minus
	404854	7143420	Plus
	404140	9843520	Plus
	401061	3242744	Minus
65	401353	9931295	Minus

70

Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-1/Lu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75

TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

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Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Tblx: Unigene gene list
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosidase, alpha-1, 2-sialidase	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel, claudin 1	14.52
	445787	U67167	Hs.315	NM_02457:Homo sapiens mucin 2, intestinal	14.04
	431912	AI650552	Hs.356183	Ha.356183:ESTs, Weakly similar to G3B4_H	14.02
	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease inhibitor, claudin-like 17	13.72
10	405690	M29540	Hs.220529	{focuslink}NM_004353:Homo sapiens carcin	13.44
	418406	X73501	Hs.84905	Ha.84905:cyclotraxin 20	12.70
	406657	M12523			12.42
	416768	AA363733	Hs.1032	NM_008507:Homo sapiens regenerating islet	11.98
	437935	AW839591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithelial	11.58
15	422578	AF239566	Hs.1545	NM_001804:Homo sapiens caudal type homeobox	11.50
	418888	AJ076801	Hs.889436	NM_004063:Homo sapiens cadherin 17, L1 c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metalloproteinase 1	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AI97275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
20	441031	AJ110884	Hs.7645	NM_005141:Homo sapiens fibrinogen, B beta chain	9.69
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.74466	Ha.572:orosomucoid 1	9.20
	407243	AA058357	Hs.74466	{focuslink}NM_006890:Homo sapiens carcin	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier family 15 (SLC15), member 1	8.69
	430178	AW49612	Hs.152475	Ha.152475:ESTs	8.51
	423673	BE003054	Hs.1685	NM_002426:Homo sapiens matrix metalloproteinase 1	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical protein	8.17
	409683	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small intestine	8.08
	450585	L15533	Hs.423	NM_138938:Homo sapiens pancreatic-esso	8.05
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (MPR1)	7.95
	436524	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid binding protein 1	7.74
	410407	XG6839	Hs.63287	NM_001216:Homo sapiens carbonic anhydrase	7.46
35	431719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible cytokine gene 1	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mRNA	7.40
	412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-III	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	NM_003002:ubiquitin-conjugating enzyme E2	7.31
40	405741	AA058357	Hs.74466	{focuslink}NM_006890:Homo sapiens carcin	7.26
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP)	7.21
	404519				7.18
	413585	AJ133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma chain	7.13
	422281	M36893	Hs.346935	NM_00613:Homo sapiens hemopexin (HPX)	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglobulin	7.02
	430828	AJ763257	Hs.86327	Ha.86327:homeobox B9	6.83
	433927	AJ557019	Hs.116467	NM_032391:Homo sapiens small nuclear protein 032391	6.81
	406587	M31126	Hs.352054	NM_352054:pregnancy specific beta-1-glycoprotein	6.78
	423538	AW803823	Hs.146268	Ha.146268:ESTs, Weakly similar to C71400	6.63
50	434206	AW136973	Hs.362915	NM_362915:Homo sapiens cDNA FLJ34876	6.37
	409041	AB033025	Hs.50081	NM_50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	NM_120879:Homo sapiens, clone MGC-32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (recombinant)	6.01
55	421964	X73079	Hs.288579	NM_026444:Homo sapiens polymeric immunoglobulin A	6.00
	430272	X04898	Hs.237658	NM_237658:apolipoprotein A-II	5.97
	413881	U01910	Hs.75599	{focuslink}NM_004488:Homo sapiens serine	5.94
	420923	AF097021	Hs.273321	NM_005418:Homo sapiens differentially expressed	5.94
	428470	AC002301	Hs.184507	NM_184507:Homo sapiens, similar to Homol	5.90
60	420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	NM_61311:ESTs, Weakly similar to 610590	5.89
	431727	AW293464	Hs.162031	NM_162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007328:Homo sapiens deleted in malignant	5.84
	432023	AW273128	Hs.300268	NM_300268:EST	5.75
65	447033	A1357412	Hs.157601	NM_157601:ESTs	5.69
	411734	AW374954	Hs.71779	NM_71779:ESTs, Weakly similar to S24C_AR	5.69
	408665	M18728		{focuslink}NM_02483:Homo sapiens carcin	5.55
	428753	AW939262	Hs.192927	NM_017726:Homo sapiens protein phosphatase 1	5.48
	443247	BE614387	Hs.333893	NM_333893:cell division cycle associated	5.45
70	409153	W03754	Hs.60813	NM_017625:Homo sapiens integrin-linked kinase (ITLN)	5.44
	449388	H53191	Hs.36723	NM_36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW812795	Hs.337534	NM_337534:Homo sapiens cDNA FLJ25241	5.38
	433013	A1697890	Hs.127337	{focuslink}NM_004855:Homo sapiens selen 2	5.38
	419079	AW014836	Hs.18844	NM_18844:ESTs	5.37
75	428355	BE266452	Hs.2257	NM_000838:Homo sapiens vitronectin (secreted)	5.35
	422956	BE545072	Hs.122579	{focuslink}NM_018098:Homo sapiens epiphysis	5.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysin	5.30
	450543	A1394037	Hs.170295	NM_170295:Homo sapiens cDNA: FLJ22090	5.30
	428187	A1687303	Hs.285529	NM_285529:G protein-coupled receptor 49	5.30
80	435538	AB011540	Hs.4930	NM_4930:low density lipoprotein receptor	5.28
	411825	AK000334	Hs.352415	NM_017787:Homo sapiens solute carrier family 16 (SCL16), member 1	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 open reading frame 1	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiogenesis 1 can	5.26
	414816	Y13703	Hs.77399	NM_001265:Homo sapiens caudal type homeobox	5.21
	430577	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG)	5.16

	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	5.12
5	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	5.06
	452194	AI694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.108358	Hs.109358:ATPase, Class V, type 10B	4.99
	408399				4.98
10	403220				4.94
	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
	416214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	4.92
	431330	X68532	Hs.2777	NM_002215:Homo sapiens Inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	4.84
15	452594	AI076405	Hs.29961	Hs.29981:acute care family 26 (scfia	4.81
	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
	446666	BE293347	Hs.11638	(focuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78819	(focuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
20	458630	AV655701	Hs.76183	NM_000773:Homo sapiens cytochrome P450,	4.78
	422310	AA316522	Hs.98370	(focuslink)NM_030622:Homo sapiens cytoch	4.78
	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens exin 2 conductin	4.75
	422330	D30763	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	4.73
	408908	BE296227	Hs.250822	(focuslink)NM_003168:Homo sapiens serine	4.70
25	423936	U77629	Hs.135639	NM_005170:Homo sapiens acbete-scute com	4.70
	404661				4.68
	408704	AA056635	Hs.5366	NM_130053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (0 Isof	4.61
30	427508	AK000134	Hs.179100	NM_017678:Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
	453894	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408903	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
35	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (a	4.54
	434540	NM_016045	Hs.3945	NM_018045:Homo sapiens chromosome 20 ope	4.54
	407242	M18728		(focuslink)NM_002463:Homo sapiens carcin	4.53
	458748	AI361530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
40	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	4.50
	411975	AI916058	Hs.144563	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
	425371	D49441	Hs.155981	NM_005820:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50620	Hs.50820:hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
45	419559	Y07828	Hs.91098	NM_007028:Homo sapiens tripartite motif-	4.44
	430294	AI536226	Hs.32976	(focuslink)NM_004485:Homo sapiens guanin	4.42
	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
50	434414	AI798376		AF134163:Homo sapiens Human endogenous r	4.36
	443426	AF098158	Hs.9329	(focuslink)NM_012112:Homo sapiens chromo	4.35
	422539	AJ009938	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
55	403055				4.31
	414808	AI434698	Hs.77356	Hs.77358:transferrin receptor (p80, CD71	4.31
	400955				4.30
	432024	AA616335	Hs.356654	NM_002083:Homo sapiens hypothetical protein FLJ32334	4.29
	432878	AF126743	Hs.279884	Hs.013238:Homo sapiens DNAJ domain-conta	4.29
60	417931	W95842	Hs.82981	Hs.82981:Homo sapiens, clone MGC-22588 I	4.28
	430832	AJ073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
	408482	NM_000576	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(focuslink)NM_025130:Homo sapiens hypoth	4.27
	452840	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
65	439211	AI890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
	459293	BE094291	Hs.155551	NM_021784:Homo sapiens hepatocyte nuclea	4.26
	449720	AJ311152	Hs.288708	(focuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.690909	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	4.24
70	421777	BE568208	Hs.108196	NM_016095:Homo sapiens HSPC037 protein (4.21
	419396	BE268326	Hs.90280	Hs.90280:5-aminoimidazole-4-carboxamide	4.20
	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.19
75	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
	426227	U67058	Hs.154299	(focuslink)NM_005242:Homo sapiens coagul	4.19
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351639	Hs.124660	Hs.124660:ESTs. Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297:Homo sapiens protein expressed	4.17
	44075	U11862	Hs.75741	NM_001091:Homo sapiens amilofide binding	4.17
	444151	AW972917	Hs.128749	(focuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125808	Hs.125808:ESTs	4.16
	445664	AB028957	Hs.12696	Hs.12896:KIAA1034 protein	4.16
80	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

	401866				4.11
	431611	U58766	Hs.264428	Hs.264428:issue specific transplantatio	4.10
	430187	A1799309	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37836 f1	4.10
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	4.08
5	449281	AI808699	Hs.162717	NM_032756:Homo sapiens hypothetical prot	4.08
	449722	BE280074	Hs.23960	Hs.23980:cyclin B1	4.08
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
	435066	BE261750	Hs.4747	NM_001353:Homo sapiens dyskeratosis cong	4.05
10	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	4.04
	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidopeptida	4.03
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine decide	4.01
15	439759	AL358065	Hs.67709	Hs.67709:Homo sapiens mRNA full length i	4.00
	441362	BE614410	Hs.23044	NM_080568:Homo sapiens similar to RIKEN	3.99
	417900	BE250127	Hs.82906	Hs.82906:CDC20 cell division cycle 20 hom	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
	456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
20	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGCI4141	3.98
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	433437	TI0536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
25	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
	428534	NM_001639	Hs.1857	Hs.1957:amyloid P component, serum	3.96
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
30	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	3.94
	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 f1	3.94
	412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
	433323	AA805132	Hs.159142	Hs.159142:junctophilic fringe homolog (Drosop	3.94
	422615	AW500470	Hs.117950	Hs.117950:phosphoribosylaminoimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
35	418113	AI272141	Hs.83464	Hs.83484:SRY (sex determining region Y)-	3.91
	433083	AL042769	Hs.191762	Hs.191762:hypothetical protein MGCI2058	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
	453439	AJ572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
	441888	AJ733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
40	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
	425234	AW152225	Hs.165909	Hs.165909:ESTs, Weakly similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(focusIn)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D31382	Hs.56325	NM_019894:Homo sapiens transmembrane pro	3.85
	436251	BE515065	Hs.296585	(focusIn)NM_006392:Homo sapiens nucleo	3.85
45	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in ml	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic ente	3.83
	430680	AW136724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130888	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	3.82
	436481	AA379597	Hs.5199	NM_014178:Homo sapiens HSPC150 protein s	3.82
	453700	AB009426	Hs.560	NM_016444:Homo sapiens apolipoprotein B	3.81
	410619	BE512730	Hs.65114	Hs.65114:keratin 18	3.81
	409420	Z15008	Hs.54451	NM_005662:Homo sapiens laminin, gamma 2	3.79
55	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	3.78
	453957	AW009077	Hs.232947	He.232947:ESTs	3.78
	428106	AJ578765	Hs.21812	He.21812:ESTs	3.78
60	434170	AA526509	Hs.159542	(focusIn)NM_001490:Homo sapiens glucos	3.78
	418322	AA284168	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
	444381	BE387335	Hs.283713	NM_138465:Homo sapiens collagen triple h	3.74
	419228	AI827237	Hs.362919	Hs.362919:ESTs	3.74
	437158	AI916600	Hs.121194	He.121194:Homo sapiens cDNA: FLJ21669 f1	3.74
65	452833	BE559681	Hs.30736	(focusIn)NM_015201:Homo sapiens block	3.73
	426831	BE296216	Hs.172673	NM_000687:Homo sapiens S-adenosylhomocys	3.73
	428970	BE276891	Hs.194691	NM_003978:Homo sapiens retinoic acid Ind	3.72
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	3.71
	408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457 f1,	3.71
	440300	N39760	Hs.8859	NM_138793:Homo sapiens myrpsin (SHAPY),	3.71
70	425976	C75094	Hs.334514	NM_026257:Homo sapiens chromosome 5 oper	3.71
	432575	AA553722	Hs.194346	Hs.194346:Spin-2 protein	3.71
	412104	AW205197	Hs.240851	(focusIn)NM_031120:Homo sapiens naked	3.71
	417001	AU076568	Hs.80741	NM_000292:Homo sapiens propionyl Coenzym	3.69
	421225	AA483798	Hs.102696	Hs.102696:MCT-1 protein	3.69
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
75	428330	L22524	Hs.2256	NM_002423:Homo sapiens matrix metallopro	3.67
	447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
	423349	AF010258	Hs.127428	NM_002142:Homo sapiens homeo box A9 (HOX	3.67
	422026	U80736	Hs.110826	Hs.110826:trinucleotide repeat containin	3.66
	419574	AI001989	Hs.51165	Hs.91185:hypothetical protein FLJ11127	3.66
80	417720	AA205625	Hs.208067	Hs.208067:ESTs	3.66
	411257	AA628987	Hs.116274	Hs.115274:Indian hedgehog homolog (Dros	3.66
	421515	Y11339	Hs.105352	(focusIn)NM_018414:Homo sapiens GalNAc	3.65
	433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs_12680:Homo sapiens cDNA FLJ10196 fis,	3.64
	412140	AA218691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
5	420542	NM_000505	Hs.1321	NM_000605:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs_6566:thyroid hormone receptor Interac	3.63
	414798	A286323	Hs.97411	Hs_97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs_2316:SRV (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs_283552:hypothetical protein BC016153	3.62
10	412056	T26160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401619				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prolif	3.58
15	413936	AF113676	Hs.297681	NM_002935:Homo sapiens serine (or cyste	3.58
	424544	M88700	Hs.160403	NM_00790:Homo sapiens dopa decarboxylas	3.58
	431563	A1027643	Hs.120912	Hs_120912:ESTs	3.57
	436602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	A1650363	Hs.116462	Hs_116462:ESTs	3.57
	439963	AW247529	Hs.6793	Hs_6793:platelet-activating factor acetyl	3.56
20	447334	AA515032	Hs.91109	Hs_91109:ESTs, Weakly similar to pulifer	3.56
	422150	A857118	Hs.279607	Hs_279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450863	A93540	Hs.25292	Hs_25292:ribonuclease H2, large subunit	3.56
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_031168:Homo sapiens baculovirus IAP r	3.55
	422105	DB4239	Hs.111732	NM_03890:Homo sapiens IgG Fe binding pr	3.55
	422532	AL006726	Hs.118126	(locuslink)NM_000308:Homo sapiens protec	3.55
	425880	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24988	Hs_24988:hypothetical protein BC016683	3.55
30	437385	W52452	Hs.356768	Hs_356768:Homo sapiens mRNA; cDNA DKFZp7	3.54
	416927	A1120168	Hs.76919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020544	Hs.14945	Hs_14945:fatty-acid-Coenzyme A ligase, t	3.53
	432378	A493046	Hs.146133	Hs_146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
35	415099	A192170	Hs.677917	NM_005002:Homo sapiens ubiquitin carboxy	3.51
	414918	A219207	Hs.72222	Hs_72222:fur-1-like 4 (C. elegans)	3.51
	440340	AW895503	Hs.125276	Hs_125276:Homo sapiens cDNA FLJ26833 fis	3.51
	418384	AW149266	Hs.25130	Hs_25130:Homo sapiens cDNA FLJ14923 fis,	3.51
40	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
	429833	NM_012079	Hs.286627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	409231	AA446644	Hs.592	NM_022354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.280855	(locuslink)NM_145175:Homo sapiens NSE1 (3.50
	453883	A1638516	Hs.347524	Hs_347524:Homo sapiens, clone MGC:24665	3.60
	442700	A3776718	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
45	410237	A7650589	Hs.61258	Hs_61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442923	AW248322	Hs.95835		3.49
50	431648	A834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_198805:Homo sapiens family with seque	3.48
	448993	A471630	Hs.355952	NM_355952:ESTs, Weakly similar to Q90320	3.48
	447320	A675419	Hs.164464	Hs_164464:Homo sapiens, clone MGC:23655	3.48
	414108	A1287592	Hs.75761	NM_003137:Homo sapiens SFRS protein kin	3.47
	420996	A0091927	Hs.100896	(locuslink)NM_018089:Homo sapiens hypoth	3.47
	439580	AF086401	Hs.293847	Hs_293847:ESTs	3.46
55	422158	L10343	Hs.112341	NM_002630:Homo sapiens protease inhibito	3.46
	418256	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_008713:Homo sapiens activated RNA pol	3.46
60	406709	A1355761	Hs.242463	Hs_242463:keratin 8	3.46
	453751	R36752	Hs.101282	Hs_101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZp58400823 pro	3.45
	416164	AW084352	Hs.157123	Hs_157123:ESTs	3.45
	405451				3.44
65	414361	A086138	Hs.204044	Hs_204044:ESTs	3.44
	422237	M19149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphofibrolysi	3.44
	457001	J03258	Hs.2062	Hs_2062:vitamin D (1,25-dihydroxyvitam	3.43
	450983	AA305384	Hs.25740	NM_014584:Homo sapiens ER01-like (S. cer	3.43
70	421828	AW891965	Hs.367942	Hs_367942:Homo sapiens, clone IMAGE:4701	3.42
	418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren's	3.42
	417348	A040507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_0020506:Homo sapiens glutathione-fructo	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
	425873	NM_013390	Hs.160417	Hs_160417:transmembrane protein 2	3.41
75	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437675	AW854365	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-sph	3.40
	439955	AW203959	Hs.149532	Hs_149532:ESTs	3.40
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium Interne	3.40
80	435745	AW967059	Hs.374342	Hs_374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413016	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs_155324:matrix metalloproteinase 11 (s	3.39

	42996	AF006005	Hs.154104	NM_002657:Homo sapiens plasmidic adan	3.38
	402944				3.37
	417165	R80137	Hs.302738	Ha.302738:Homo sapiens cDNA: FLJ21426 fl	3.37
	427528	AU077143	Hs.178585	NM_002388:Homo sapiens MCM3 minichromosome	3.37
5	426711	AA383471	Hs.343800	(focuslink)NM_033255:Homo sapiens epith	3.37
	439186	AI697274	Hs.105435	Ha.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bl	3.36
	426174	AA547959	Hs.115838	Ha.115838:ESTs	3.36
10	421585	U95526	Hs.302043	NM_003955:Homo sapiens chemokine (C-C mo	3.36
	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.165320	NM_002968:Homo sapiens small Inducible c	3.36
	438746	AI885615	Hs.184727	Ha.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome profil	3.34
	456946	T29678	Hs.166068	Ha.166068:willin 1	3.33
	425580	L11144	Hs.1907	Ha.1907:galanin	3.33
	412605	AW410734	Hs.74111	Ha.74111:RNA binding protein (autointiga	3.33
20	441384	AA447849	Hs.288660	Ha.288660:Homo sapiens cDNA: FLJ22182 fl	3.33
	416782	L35035	Hs.79886	(focuslink)NM_144563:Homo sapiens ribose	3.33
	426761	AI015709	Hs.172089	Ha.172089:pro-oncrosis receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_014131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Ha.194366:transferrin (prealbumin, amy	3.31
25	431192	AI670056	Hs.137274	Ha.137274:ESTs, Weakly similar to hypoth	3.30
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Ha.118727:Homo sapiens cDNA FLJ33803 fis	3.30
	410639	BE265047	Hs.65234	(focuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Ha.63325:transmembrane protease, serine	3.29
30	410850	AW362867	Hs.302738	NM_002738:Homo sapiens cDNA: FLJ21426 fl	3.29
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryo	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
35	434031	BE384165	Hs.23723	(focuslink)NM_025215:Homo sapiens pseudo	3.28
	421975	AW961017	Hs.6459	(focuslink)NM_024531:Homo sapiens hypoth	3.28
	452299	AW206330	Hs.355663	Ha.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Ha.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Ha.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(focuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Ha.4867:memannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_031100:Homo sapiens MT-protochain	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Ha.90073:CEST1 chromosome segregation 1	3.27
	414695	BE439915	Hs.76913	Ha.76913:proteasome (prosome, macropain)	3.27
45	444371	BE640274	Hs.239	Ha.239:forkhead box M1	3.27
	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kO	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens stathmin 1 (lyso	3.27
	403485				3.27
50	441623	AA315805	Hs.348710	Ha.348710:Homo sapiens, clone IMAGE:4242	3.26
	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435949	BE306242	Hs.16098	Ha.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-tRN	3.26
	404684				3.25
55	447188	H66423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Ha.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75263	NM_004135:Homo sapiens Isocitrate dehydr	3.24
	424243	AI949389	Hs.143600	Ha.143600:gaigi phosphoprotein 4	3.24
60	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
	452281	T93500	Hs.28792	Ha.28792:Homo sapiens cDNA FLJ11041 fis	3.24
	418065	BE267931	Hs.78996	NM_002692:Homo sapiens proliferating cel	3.23
	427333	AF057797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
65	432035	AA524725	Hs.162108	Ha.162108:ESTs	3.23
	408888	AW292286	Hs.255058	Ha.255058:ESTs	3.23
	429504	X39133	Hs.204238	Ha.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW136561	Hs.181245	Ha.181245:Homo sapiens cDNA FLJ12532 fis	3.22
	426991	AK001536	Hs.214410	Ha.214410:Homo sapiens cDNA FLJ31573 fis	3.22
70	408901	AK001330	Hs.48856	(focuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW800291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Ha.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
	414639	X57055	Hs.76715	NM_002217:Homo sapiens pre-alpha (globul	3.21
75	439975	AW328081	Hs.5817	NM_033453:Homo sapiens inosine triphosph	3.20
	444281	AA298958	Hs.10724	Ha.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box H39 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
	427747	AW411425	Hs.180655	(focuslink)NM_004217:Homo sapiens serine	3.20
80	436469	AK001455	Hs.5198	Ha.5198:Down syndrome critical region ge	3.19
	400130		Hs.155580	NM_001746:Homo sapiens calcinin (CANX),	3.19
	422283	X94453	Hs.114366	Ha.114366:pyruvate-5-carboxylate synthe	3.19
	400290	H18836	Hs.31608	(focuslink)NM_017835:Homo sapiens transl	3.18

	419239	AA468183	Hs.335798	(locuslink)NM_033103:Homo sapiens rhophil	3.18
	426215	AW863419	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
5	413313	NM_002047	Hs.293985	NM_002047:Homo sapiens glycyl-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015969:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22786	Hs.62407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426088	AF038007	Hs.166196	NM_006033:Homo sapiens ATPase, Class I,	3.16
	416864	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mastenochymal stem	3.16
	406708	A1282759		AT282759:qB4a01.x1 NCI_CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
15	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.15
20	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:coxackievirus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	436636	AA531276	Hs.55509	Hs.55509:ESTs, Weakly similar to similar	3.15
25	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fs	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylneuramini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antigen	3.14
30	417791	AW965339	Hs.44259	Hs.44259:Homo sapiens cDNA FLJ37972 fs,	3.14
	417115	AW952792	Hs.334812	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.66879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	458906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutase	3.13
35	408056	AA312329	Hs.42331	Hs.42331:apoflin-A4	3.13
	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AB228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50984	(locuslink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	M86698	Hs.169840	Hs.169840:TTK protein kinase	3.11
	408152	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulphatase E (3.10
45	434861	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens deimocollin 2 (DS	3.10
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27495	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW7592256	Hs.91011	NM_063408:Homo sapiens anterior gradient	3.09
	416591	AW752368	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fs,	3.08
	422163	AF027208	Hs.112360	Hs.112360:plummet-like 1 (mouse)	3.08
	447760	AI431328	Hs.348605	NM_052963:Homo sapiens mitochondrial top	3.08
55	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410168	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
	422880	A228704	Hs.193974	Hs.193974:glutathione reductase	3.08
60	442013	AA506476	Hs.375009	NM_376009:Homo sapiens mRNA; cDNA DKFZp6	3.08
	431722	AF161528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421505	BE3027956	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to T0629t	3.07
65	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412630	AE768268	Hs.266273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW951952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12663 fs	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_002659	Hs.178557	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW138099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ26888 fs	3.05
	431945	AW00827	Hs.11952	NM_030761:Homo sapiens apoptosis regulat	3.05
	435703	AW530133	Hs.83313	(locuslink)NM_020192:Homo sapiens GKO03	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fs	3.04
	403739				3.04
75	444664	N25362	Hs.11615	NM_016088:Homo sapiens map kinase phosph	3.04
	409152	AA176586	Hs.194346	Hs.194346:Spir-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein {L	3.04
	406545				3.03
80	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGCG322	3.03
	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434623	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens sltu	3.03
	440088	BE559877	Hs.183232	NM_024639:Homo sapiens hypothetical prot	3.02

	414907	X90725	Hs.77597	NM_000898:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGCI3170	3.02
	434203	BE282677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
5	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
10	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (3.01
	426031	AA295251	Hs.168066	(locuslink)NM_008697:Homo sapiens clepla	3.01
	417678	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2',5'-	3.01
	417366	AL037228	Hs.301957	NM_018144:Homo sapiens Sac61 alpha form	3.00
	429893	W92620	Hs.280855	(locuslink)NM_145175:Homo sapiens NSE1 (3.00
15	417526	AA568906	Hs.82240	Hs.82240:syntactic 3A	3.00
	414732	AW410976	Hs.77152	Hs.77152:MCMT mithochromosome maintenance	3.00
	409614	BE297412	Hs.65189	NM_016489:Homo sapiens 6'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411056	U80034	Hs.88583	NM_005932:Homo sapiens mitochondrial int	2.99
20	433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to 13	2.99
	420767	AF072711	Hs.59918	Hs.59918:carboxyl ester lipase (feline sal	2.99
	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.98808	Hs.98808:hypothetical protein FLJ20485	2.99
25	413380	AI904232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	N71826	Hs.105485	NM_003085:Homo sapiens small nuclear rib	2.99
	439352	BE5614347	Hs.168915	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fl	2.98
	431193	AW749505	Hs.286770	Hs.286770:KIAA1719 protein	2.98
30	457211	AW972565	Hs.32399	(locuslink)NM_145240:Homo sapiens simila	2.88
	410467	AF102548	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
	422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
	416526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012489:Homo sapiens chromosome 20 ope	2.97
35	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M98956	Hs.75581	NM_003212:Homo sapiens teratocarcinoma-d	2.97
	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
	417911	AA333387	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
40	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409556	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A {	2.96
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
	418245	AA088757	Hs.83883	NM_020162:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
45	421953	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
	459306	AW578452	Hs.5072	AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
	425209	AL049761	Hs.155140	NM_0018895:Homo sapiens casein kinase 2,	2.96
	439559	AW870780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
	408683	R56666	Hs.46847	NM_016814:Homo sapiens TRAF and TNF rece	2.95
50	432843	BE250865	Hs.279529	NM_013237:Homo sapiens px19-like protein	2.95
	406684	X16354	Hs.50884	(locuslink)NM_001712:Homo sapiens carcin	2.95
	410006	AW352308	Hs.163900	Hs.57783:Homo sapiens eukaryotic transl	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ep	2.94
55	449437	A702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
	446695	AF279265	Hs.298478	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.93859	(locuslink)NM_004911:Homo sapiens protei	2.93
60	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter sf	2.93
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
	409012	AI117435	Hs.49725	Hs.49725:DKFZP434/216 protein	2.93
65	428048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	425373	U80082	Hs.169500	Hs.169500:KIAA0826 protein	2.92
	422397	AJ223366	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037655	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	422639	AK001639	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
70	443715	AI583187	Hs.9700	NM_001236:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	2.92
	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_008420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
75	429628	U36787	Hs.211571	NM_005333:Homo sapiens holoxyochrome c	2.92
	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
	400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
	410381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
80	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

	433487	U31814	Hs.3352	NM_001527:Homo sapiens histone deacetylase	2.91
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear ribonucleoprotein polypeptide K2	2.90
	430287	AW182459	Hs.125759	Hs.125759:likely ortholog of mouse RING finger protein 121	2.90
5	434026	R15486	Hs.285218	(locuslink)NM_021213:Homo sapiens phosphatase, dual specificity, mitogen-activated protein kinase kinase kinase 6	2.90
	447698	AJ420156	Hs.328733	NM_052856:Homo sapiens similar to RIKEN C026044L03.1	2.90
	411263	BE297802	Hs.69360	NM_008845:Homo sapiens kinesin-like 6 (mRNA)	2.90
	432754	BE241691	Hs.3100	Hs.3100:lysyl-tRNA synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046:Homo sapiens exosomal core protein 10	2.90
	420421	AF281133	Hs.343589	Hs.343589:exosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading frame 184062	2.89
	414420	AA043424	Hs.76095	NM_052845:Homo sapiens immediate early gene 5	2.89
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg6, S. cerevisiae homolog	2.89
15	401405				2.89
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	2.89
	400247		Hs.356473	NM_006713:Homo sapiens activated RNA polymerase III	2.89
	421910	NM_014566	Hs.109437	NM_014566:Homo sapiens hormonally upregulated protein	2.89
	413610	AL117554	Hs.119808	NM_015934:Homo sapiens nucleolar protein 1	2.89
20	413588	AA971014	Hs.754532	NM_008843:Homo sapiens IMP (inosine monophosphate) kinase	2.89
	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription factor 1	2.88
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated protein kinase kinase kinase 1	2.88
	417634	W27202	Hs.82327	NM_000178:Homo sapiens glutathione synthetase	2.88
	435099	AC004770	Hs.4755	NM_004111:Homo sapiens flap structure-splicing factor 1	2.88
25	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha 1	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207:Homo sapiens cleavable secretory protein 1	2.88
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding protein	2.88
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenase 1	2.88
	407770	AV607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN15)	2.88
30	408847	AV290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988	2.87
	448250	NM_016034	Hs.20778	(locuslink)NM_016034:Homo sapiens mitochondrial tRNA	2.87
	428810	AF069238	Hs.193788	NM_006251:Homo sapiens nitric oxide synthase	2.87
	427505	AA361562	Hs.178761	NM_178761:26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146:v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	2.87
	409262	AK000631	Hs.52256	Hs.52256:hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	2.87
	450378	AV249181	Hs.154796	Hs.154796:Homo sapiens cDNA FLJ37976	2.86
	411761	A173848	Hs.71935	NM_021220:Homo sapiens zinc finger protein 173	2.86
40	415681	AW963979	Hs.24723	Hs.24723:ESTs	2.86
	417715	AV969587	Hs.86386	Hs.86386:ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931:hypothetical protein FLJ10607	2.86
	436138	H5323	Hs.25717	Hs.25717:Homo sapiens cDNA: FLJ23454	2.86
	432858	BE818609	Hs.279591	Hs.279591:Homo sapiens, Similar to RNA polymerase II subunit 10	2.86
45	434457	AF141332	Hs.200333	NM_016690:Homo sapiens apolipoprotein B48	2.86
	444237	AA336878	Hs.9842	Hs.9842:ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nucleophosmin	2.85
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, protein	2.85
	424270	AK001818	Hs.144407	NM_016283:Homo sapiens hypothetical protein	2.85
50	414396	BE548266	Hs.76057	(locuslink)NM_000403:Homo sapiens galactose-3-O-sulfotransfase	2.85
	426120	AA325243	Hs.166887	Hs.166887:coxin 1	2.85
	446663	AA614599	Hs.356501	(locuslink)NM_032335:Homo sapiens hypothetical protein	2.85
	443802	AW504924	Hs.9805	Hs.9805:expartin 5	2.85
55	445863	R12234	Hs.13396	Hs.13396:Homo sapiens clone 25028 mRNA	2.85
	434808	AF155108	Hs.256150	Hs.266150:NY-REN-41 antigen	2.85
	440334	BE275112	Hs.7165	NM_003904:Homo sapiens zinc finger protein	2.85
	449057	AB037764	Hs.22941	Hs.22941:KIAA1363 protein	2.85
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interferon regulatory factor 4	2.84
60	446421	BE297434	Hs.15071	Hs.15071:chaperonin containing TCP1, subunit 1B	2.84
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCE_A	2.84
	426549	U30930	Hs.158540	(locuslink)NM_003360:Homo sapiens UDP glucose 4-epimerase	2.84
	429638	A1916652	Hs.211577	(locuslink)NM_004986:Homo sapiens kinase	2.84
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphatase 1	2.84
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	2.84
65	407833	AW955632	Hs.666666	Hs.666666:chromosome 7 open reading frame	2.84
	415083	A1626833	Hs.27179	Hs.27179:Homo sapiens cDNA FLJ2933	2.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9)	2.83
	443572	AA256510	Hs.9605	Hs.9605:cleavage and polyadenylation specific protein	2.83
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN12)	2.83
70	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (LNBB3)	2.83
	453028	AB006532	Hs.31442	NM_004260:Homo sapiens RecQL helicase	2.83
	425047	U34038	Hs.164299	NM_005242:Homo sapiens coagulation factor	2.83
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN C026044L03.1	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_006518:Homo sapiens 3-hydroxy-3-methylglutaryl-coenzyme A lyase	2.83
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	2.83
75	417677	NM_016055	Hs.82389	NM_016055:Homo sapiens mitochondrial ribosomal protein L13	2.83
	425263	NM_001197	Hs.156419	NM_001197:Homo sapiens BCL2-interacting protein	2.82
	437430	W44671	Hs.124	NM_014628:Homo sapiens gene predicted from ESTs	2.82
	428289	M26301	Hs.2253	Hs.2253:complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193518	NM_003921:Homo sapiens B-cell CLL/lymphoma 10	2.82
	432633	A1796390	Hs.210667	Hs.210667:ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575:ESTs	2.82

		Hs.58189	Hs.58189:eukaryotic translation initiation	2.82	
410045	AA806930	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82	
454144	BE280478	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81	
430387	AW672884	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81	
434583	AA095761	Hs.2795	Hs.2795:alactate dehydrogenase A	2.81	
5	431512	BE270734	Hs.104830:ESTs	2.81	
	428093	AW594508	NM_012080:Homo sapiens DNA segment, nume	2.81	
	416047	BE439894	NM_004205:Homo sapiens programmed cell d	2.81	
	447495	AW401864	Hs.18720	Hs.110895:hypothetical protein MGC3133	2.81
10	452199	BE255643	Hs.110895	NM_002011:Homo sapiens fibroblast growth	2.80
	425998	AU076629	Hs.165950	NM_002157:Homo sapiens heat shock 10kD p	2.80
	445921	AW672511	Hs.153799	NM_153799:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
15	436127	W94824	Hs.11585	NM_080749:Homo sapiens chromosome 20 ope	2.80
	418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	US2112	Hs.182018	Hs.182018:interleukin-1 receptor-associ	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
20	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	2.79
	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
	418950	NM_004494	Hs.89525	{focusIn}NM_004494:Homo sapiens hepa	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
	434750	BE019254	Hs.4112	Hs.4112:complex 1	2.79
25	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
	400529				2.79
	436414	BE264633	Hs.143638	NM_033681:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	{focusIn}NM_003951:Homo sapiens protei	2.79
30	427963	AI042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (2.79
	426459	AF151812	Hs.169892	NM_015966:Homo sapiens serologically def	2.79
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
	442468	N77737	Hs.9349	NM_138933:Homo sapiens apocet-1 complex	2.79
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
35	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	{focusIn}NM_018396:Homo sapiens putat	2.79
	452875	BE275760	Hs.30328	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.01381	Hs.81381:heterogeneous nuclear ribonucle	2.79
	407811	AW190802	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
	409836	AA305729	Hs.18272	{focusIn}NM_030674:Homo sapiens solute	2.78
40	447619	A174800	Hs.19064	{focusIn}NM_018530:Homo sapiens hypoth	2.78
	434845	BE267057	Hs.325321	WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE269042	Hs.5681	Hs.9661:proteasome (prosome, macropain)	2.78
45	414045	NM_002951	Hs.75722	NM_002851:Homo sapiens ribophorin II (RP	2.78
	430512	AF1B2294	Hs.241678	NM_016200:Homo sapiens U6 snRNA-associat	2.78
	432638	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE268134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
50	448003	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
	443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	416313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF028004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
55	456950	AF111170	Hs.308165	Hs.308165:ESTs, Highly similar to unkno	2.77
	432543	AA652690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fis	2.77
	423271	W47225	Hs.128256	NM_000578:Homo sapiens Interleukin 1, be	2.77
	410695	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte aci	2.77
60	457757	AA434108	Hs.12271	NM_012182:Homo sapiens F-box and leucine	2.77
	420186	NM_015925	Hs.95697	Hs.95697:iver-specific bHLH-Zip transcr	2.77
	410094	BE174897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
65	432705	AI073473	Hs.157123	Hs.157123:ESTs	2.77
	445658	AI440137	Hs.164989	NM_138492:Homo sapiens hypothetical prot	2.76
	419485	AA489023	Hs.99807	NM_99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
	432898	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	420438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
70	414767	BE541581	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	406830	AI028848	Hs.342389	Hs.342389:peptidyl/prolyl isomerase A (cy	2.76
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	{focusIn}NM_015913:Homo sapiens hypoth	2.76
	433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
75	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
	446946	AI078932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
80	433862	D86560	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
	417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416186	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication init	2.75	
407971	A1469117	Hs.62918	Hs.62918:CD981 cell division cycle 91-II	2.75	
432403	AA550815	Hs.124840	(focuslink)NM_139456:Homo sapiens hypoth	2.75	
410775	AB014460	Hs.66196	NM_002528:Homo sapiens nth endonuclease	2.75	
5	444197	BE269947	Hs.10590	NM_018833:Homo sapiens zinc finger prote	2.75
	447250	A1878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	ALQ80088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
10	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	2.74
	426235	A1631964	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fs,	2.74
	413186	AU077147	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW988058	Hs.92381	NM_019094:Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.69461:DKFZP434C246 protein	2.74
15	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	A1064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
20	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	2.73
	444706	AK000398	Hs.11747	(focuslink)NM_017798:Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_006889:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fs	2.73
25	452461	B67223	Hs.108106	Hs.108106:ubiquitin-like, containing PHD	2.73
	407699	AA285974	Hs.26246	NM_024622:Homo sapiens hypothetical prot	2.73
	412258	AA375768	Hs.98125	(focuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fs,	2.72
	443905	A1215948	Hs.143959	Hs.143959:ESTs	2.72
30	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone fami	2.72
	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
	424685	W21223	Hs.161734	Hs.161734:nuclear transport factor 2	2.72
	424692	AA429634	Hs.151791	NM_014678:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_0020142:Homo sapiens FK506 binding pro	2.72
35	418054	AA02318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	2.72
	450164	A1239923	Hs.63931	NM_087759:Homo sapiens diaphus homolog	2.71
	421115	AK001763	Hs.73229	Hs.73229:hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_0140173:Homo sapiens HSPC003 protein (2.71
	447349	A1375546	Hs.24763	BE743847:601577765F1 NIH_3MG_C_9 Homo sapi	2.71
40	445413	AA151342	Hs.12677	(focuslink)NM_016077:Homo sapiens CGI-14	2.71
	448826	A1508252	Hs.255585	Hs.255585:Homo sapiens cDNA FLJ33892 fs	2.71
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	2.71
	441020	W79263	Hs.35962	W79263:Homo sapiens mRNA; cDNA DKFZp68	2.70
45	458933	A1638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
	430462	A1684156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439656	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fs	2.70
	425236	AW087800	Hs.155223	NM_003714:Homo sapiens stannicocalchin 2 (2.70
50	420085	A7141809	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14162 fs,	2.70
	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW975531	Hs.164443	Hs.164443:MCMA4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_016939:Homo sapiens CGI-09 protein (L	2.70
55	421344	AD631030	Hs.103865	(focuslink)NM_015873:Homo sapiens villin	2.70
	446607	A1681065	Hs.155780	Hs.155780:ESTs	2.70
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347:Homo sapiens popofyl probil	2.70
	413794	AF234532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
60	451484	A100228	Hs.295868	(focuslink)NM_030974:Homo sapiens hypoth	2.70
	458820	A6562161	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	Hs.97997	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AAT678406	Hs.8854	Hs.8854:Putl oncogene homolog, MYC activ	2.69
65	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_0221451:Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551:Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452:Homo sapiens phosphatocystam	2.69
	416084	L16991	Hs.79008	NM_0121452:Homo sapiens deoxythymidylate	2.69
	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
70	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
	424373	AJ133798	Hs.146218	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	A1418609	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interferon enhancer binding fa	2.69
	420062	AW411096	Hs.84785	(focuslink)NM_021809:Homo sapiens TGFB-1	2.69
75	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016626	Hs.181361	Hs.191381:hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001981:Homo sapiens eukaryotic transl	2.68
	421933	R89861	Hs.109655	NM_006746:Homo sapiens sex comb on middle	2.68
80	417750	A1287720	Hs.265023	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425601	AW628485	Hs.140720	NM_012083:Homo sapiens frequently restra	2.68

	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenance	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406573	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
5	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	2.68
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhiblin, beta C (2.68
	427719	A1393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 (2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
10	413142	M81740	Hs.75212	(locuslink)NM_002539:Homo sapiens ornith	2.67
	414998	NM_002543	Hs.77723	NM_002543:Homo sapiens oxidized low dens	2.67
	432391	A1732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
15	418738	AV398633	Hs.6582	Hs.6582:solute carrier family 7, (cation	2.67
	439586	AA822936	Hs.110039	Hs.110039:ESTs	2.67
	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
20	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	2.67
	445304	BE813206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 (s	2.67
	417601	NM_014735	Hs.822292	NM_014735:Homo sapiens KIAA0215 gene pro	2.68
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AB65664	Hs.351863	(locuslink)NM_003312:Homo sapiens thioer	2.66
25	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, proti	2.66
	456248	AL035788	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427091	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
30	419705	AW368634	Hs.164331	Hs.164331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coel protein gamm	2.66
	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40389 (s	2.66
	446356	A816736	Hs.14886	Hs.14886:zinc finger, DHHC domain contai	2.66
	432435	BE218866	Hs.282070	Hs.282070:ESTs	2.66
35	433020	AJ375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436105	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
	431127	U68618	Hs.250581	Hs.250581:SWV/SNF related, matrix assoc	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
40	414761	AU077228	Hs.77258	NM_004456:Homo sapiens enhancer of zeste	2.65
	417378	N34731	Hs.74562	NM_078480:Homo sapiens fuse-blinding prot	2.65
	409893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenance	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP56411171 protein	2.64
	428072	BE259802	Hs.182366	NM_016292:Homo sapiens heat shock prote	2.64
45	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGCC2574	2.64
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 (s	2.64
	409214	AW405987	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDC28 protein kinase 1	2.64
50	433570	AI580053	Hs.109007	NM_109007:Homo sapiens, Similar to LOC16	2.64
	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (2.64
	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432984	AF116395	Hs.279885	NM_014317:Homo sapiens trans-prymarytrans	2.63
	448485	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
55	428144	BE259243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	A1694131	Hs.29002	Hs.29002:KIAA1708 protein	2.63
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37064	Hs.37054:ephrin-A3	2.63
	430024	A808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	2.63
60	406122				2.63
	420988	AW006352	Hs.159843	Hs.159843:ESTs, Weakly similar to putati	2.63
	436433	AW631437	Hs.5184	(locuslink)NM_016397:Homo sapiens TH1-ii	2.63
	417129	A138100	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.53042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
65	419420	AA355435	Hs.30724	(locuslink)NM_001566:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	2.63
	412599	AL076782	Hs.248267	(locuslink)NM_021128:Homo sapiens mercap	2.63
	436199	R38948	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 (s	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenance	2.63
70	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CD411 protein (CD	2.62
	437379	AL369575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
	409703	NM_006187	Hs.56009	Hs.56008:2'-S-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287650	NM_0022119:Homo sapiens Integral membrane	2.62
	418216	AA662240	Hs.283098	Hs.283098:AF15e14 protein	2.62
	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
75	413781	J05272	Hs.850	(locuslink)NM_00983:Homo sapiens IMP (I	2.62
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-28 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
80	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens pleck	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	445786	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis	2.62

	437033	AW248364	Hs.5409	(locuslink)NM_004975:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
5	433037	AA14158	Hs.279938	NM_014158:Homo sapiens HSPC057 protein {	2.61
	414438	AB79277	Hs.76136	(locuslink)NM_003329:Homo sapiens thiore	2.61
	416221	BE513171	Hs.73086	(locuslink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448825	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410585	AT733735	Hs.114905	NM_032366:Homo sapiens ER to nucleus sig	2.60
15	411400	AA311919	Hs.89851	NM_018983:Homo sapiens nucleolar protein	2.60
	429770	AT765047	Hs.99736	Hs.99736:hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	430237	AT772144	Hs.236522	Hs.236522:Dkf2p434p106 protein	2.60
	419507	RS2557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding cassa	2.60
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	2.60
	457234	AW966360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylgalactosamine {	2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
	438533	AA40266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
25	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372260	Hs.178576	(locuslink)NM_030877:Homo sapiens caten	2.60
	453949	AU077148	Hs.36927	(locuslink)NM_006644:Homo sapiens heat s	2.59
30	451110	AI955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.58877	Hs.58877:cyclochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	442990	AA197226	Hs.19347	NM_023351:Homo sapiens mitochondrial rib	2.59
35	424197	AF056834	Hs.142899	NM_019982:Homo sapiens germ cell specifi	2.59
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T89226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
	441153	BE562826	Hs.562826	BE562826:601336534F1 NIH_MGC_44 Homo sap	2.59
40	410570	AH133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	430315	AI638871	Hs.378955	NM_378955:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
45	449019	AI949095	Hs.67778	Hs.67778:Homo sapiens, clone IMAGE:64556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	418330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
50	437712	X04558	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.280229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
55	418803	US0079	Hs.88556	NM_004984:Homo sapiens histone deacetylase	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21768	Hs.21768:ESTs, Weakly similar to hypoth	2.57
	447418	AA063074	Hs.18552	He.18552:E24G2 protein	2.57
	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
60	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001689:Homo sapiens arylsulphatase D {	2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AI859390	Hs.298940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427678	BE257756	Hs.180312	NM_016085:Homo sapiens mitochondrial rib	2.57
	444656	AI277524	Hs.145189	He.145199:ESTs, Weakly similar to hypoth	2.57
	425206	NM_002153	Hs.155108	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0285 gene product	2.56
	427648	AI375722	Hs.180082	He.180082:proteasome (prosome, macropain	2.56
	419183	D29343	Hs.34769	NM_005216:Homo sapiens dolichyl-diphosph	2.56
70	409954	AW360228	Hs.67928	He.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcripton fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
75	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63860	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.262990	(locuslink)NM_033550:Homo sapiens chromo	2.56
	418650	BE386750	Hs.86978	He.86978:prolyl endopeptidase	2.56
	425368	A3014595	Hs.155978	(locuslink)NM_003588:Homo sapiens culin	2.56
80	420614	AL110291	Hs.93364	Hs.93364:abhydrolase domain containing 1	2.56
	427878	A1494291	Hs.369171	He.369171:ESTs	2.56
	418662	BE550964	Hs.88399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BES91787	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.56

	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
5	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ	2.55
	428410	BE29B446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400995				2.55
10	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens f5485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1258 protein	2.55
15	410012	AW015832	Hs.57898	(locuslink)NM_017619:Homo sapiens hypoth	2.55
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AB236933	Hs.323494	(locuslink)NM_017384:Homo sapiens hypoth	2.55
	418861	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinase	2.55
20	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AB161254	Hs.105196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
	446715	AJ337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_008855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal [pyrido	2.54
25	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
	409632	WT4001	Hs.55279	NM_002539:Homo sapiens serine (or cyste	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	456031	AA335896	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
30	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561810	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
	448775	AB025237	Hs.368	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	WT0171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015956:Homo sapiens mitochondrial rib	2.53
35	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Huntington	2.53
40	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14076	2.53
	417933	X02208	Hs.82962	NM_010711:Homo sapiens thymidylate synth	2.53
	426812	AF105355	Hs.172813	NM_006598:Homo sapiens solute carrier fa	2.53
	452013	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
45	409289	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI056664	Hs.31731	(locuslink)NM_012094:Homo sapiens perox	2.53
	412525	AA681439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
50	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif-	2.53
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
	434274	AA626539	Hs.57783	Hs.57783:eukaryotic translation initial	2.53
	400282		Hs.289101	NM_003113:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155337	NM_008041:Homo sapiens protein kinase, D	2.53
	453344	BE349076	Hs.44571	Hs.44571:ESTs	2.53
55	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.53
	417691	AL076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
	438012	BE383384	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI807114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	2.52
60	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
65	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AB217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
	440773	AJ352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440687	AL138481	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	2.52
70	424259	AK001778	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CD92 antigen (CD	2.52
	452204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453565	AA626280	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016658	Hs.274411	NM_016658:Homo sapiens SCAN domain conta	2.52
	433271	BE621697	Hs.14317	NM_018848:Homo sapiens nuclear protein	2.51
75	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exonuclease	2.51
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
80	429569	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0220 gene pro	2.51
	434474	AL042936	Hs.211571	(locuslink)NM_005333:Homo sapiens holocy	2.51
	424482	BE286621	Hs.149155	(locuslink)NM_003374:Homo sapiens vang	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_016386:Homo sapiens hypoth	2.51

	421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIIB	2.51
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
	452104	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
	436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
5	424909	S78187	Hs.153752	[focuslink]NM_004358:Homo sapiens cell d	2.51
	435877	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor Interac	2.51
	406363				2.51
	452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
10	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
	421837	AI878857	Hs.109706	NM_016185:Homo sapiens hematological and	2.51
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
	434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
15	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
	428053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
	432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
	452390	AI644142	Hs.29288	(focuslink)NM_022759:Homo sapiens endo-b	2.50
	429203	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inac)	2.50
20	400076				2.60
	420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
	422244	Y08890	Hs.113603	NM_002271:Homo sapiens karyopherin (Impo	2.50
	410723	AA100583	Hs.372108	Hs.372108:ESTs	2.50
	435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
25	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospho	2.50
	433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
	446391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

30	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
35	Pkey	CAT Number	Accession	
	406885	0_0	M18728	
	434414	35978_1	AF134164 BF809407 AA218557 BF842863 AI267168 BF876178 BG899263 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422	
			AA055556 BF773400 BF998669 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826631 AW754298	
40			AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI029309 BG987850 BE093176	
	432407	MH1429_12	BF854337	
			BG036676 BF772005 BF771666 BG980366 BG960381 NM_005712 AF110316 BE074534 BE182776 BE158000 BE157989 BE714315 AW818104	
			AW874519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279	
45			BE748870 BC9319540 BE748864 BF739224 BG986165 AK057263 BI861466 AA683341 AA457591 BG949264 AW392886 AA071122 AA227849	
			AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF70411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859	
			BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF745211 AA179928	
	406706	0_0	A1282750	
	459306	223120_-4	AW576452	
50	447349	1063443_1	BE743847 AW809603 BM469626 AI375546	
	441153	254480_3	BE582826 BE378727	

TABLE 10C

55	Pkey:	Unique number corresponding to an Eos probe		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1989) 402:488-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
60	Pkey	Ref	Strand	Nt_position
	404519	B152000	Plus	12817-13000
	406399	9256288	Minus	63448-63554
65	403220	7630899	Plus	64338-84517
	404661	9797073	Plus	33374-33575,33769-34008
	402496	9797769	Minus	8615-9103
	403055	8748904	Minus	109532-110226
	400955	7770578	Minus	173043-173564
70	403218	7630959	Plus	58039-58149
	401866	8018106	Plus	73126-73623
	403221	7630869	Plus	68294-664438,66936-67124
	401519	6649315	Plus	157315-157950
	405451	7622617	Minus	145949-146227
75	403532	8076842	Minus	81760-81901
	402944	9368423	Plus	110411-110716,111173-111640
	403219	7630969	Plus	61858-61985
	403381	9438267	Minus	26009-26178
	403485	9866528	Plus	2888-3001,3198-3532,3655-4117
80	405484	5922025	Plus	199214-199579,199572-199920,200262-20049
	404584	9797403	Minus	110881-111020
	402474	7547175	Minus	53526-53628,55765-55920,57530-57757
	405506	6466489	Plus	80014-80401,80593-81125
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495

406545	7711510	Plus	145662-145781,147854-147984,148098-14824
401405	7768126	Minus	69276-69452,69548-69958
400750	8119067	Plus	198991-199168,199316-199546
401179	9438647	Plus	113477-113893
5	400529	9796968	Plus 138232-138423
	403817	8952055	Plus 110297-111052
	400448	9887687	Minus 177372-177674
	406122	9144087	Minus 30940-31386
	406180	7283201	Minus 30923-39107
10	402829	8918414	Plus 101532-101852,102006-102263
	400995	8099094	Plus 141186-141601
	404826	6572184	Plus 47726-48046
	406363	9256114	Plus 14403-14602,17000-17147,17241-17368

15

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Ess-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colon-derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

25

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey:	Unique Eos probeset identifier number	ExAccn:	Exemplar Accession number, Genbank accession number	UnigeneID:	Unigene number	Unigene Title: Unigene gene title	R1:	Ratio of tumor to normal adult tissues
35	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosidase, beta-1,3- (locuslink)NM_004383:Homo sapiens carcino-embryonic antigen (locuslink)NM_002483:Homo sapiens carcino-embryonic antigen (locuslink)NM_002483:Homo sapiens carcino-embryonic antigen	37.18			
	406690	M29540	Hs.220529	(locuslink)NM_004383:Homo sapiens carcino-embryonic antigen	31.24			
	407242	M18728		(locuslink)NM_002483:Homo sapiens carcino-embryonic antigen	24.81			
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcino-embryonic antigen	20.54			
40	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	20.38			
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel, M12523	20.13			
	408687				19.89			
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithelial membrane protein (locuslink)NM_004383:Homo sapiens carcino-embryonic antigen	19.68			
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestinal	19.55			
45	423541	AA295922	Hs.129778	NM_014471:Homo sapiens serine protease i (locuslink)NM_007329:Homo sapiens deleted in malignancy 1	18.33			
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malignancy 1	17.47			
	414386	X00442	Hs.78990	NM_005143:Homo sapiens haptoglobin (HP), alpha chain	17.37			
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating islet amyloid polypeptide	16.99			
50	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeobox gene 2	15.15			
	441031	AI110884	Hs.7645	NM_006141:Homo sapiens fibrinogen, B beta chain	15.02			
	421582	AI910275	Hs.380470	NM_003225:Homo sapiens trichorhinphelin factor 1	14.23			
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcino-embryonic antigen	14.12			
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene 1	13.64			
55	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48			
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43			
	418888	AU076801	Hs.294935	NM_004063:Homo sapiens cadherin 17, L1 c	13.20			
	463863	X02544	Hs.572	Hs.572:transmembrane protein	13.06			
	413719	BE439580	Hs.76498	NM_004591:Homo sapiens small inducible cation channel protein, beta	12.58			
60	436217	T63925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34			
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	11.72			
	409153	W03754	Hs.50813	NM_017625:Homo sapiens Intelectin (ITLN)	11.72			
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with sequence similarity to 1	11.49			
	406399				11.25			
65	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglobulin-like protein	11.18			
	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunoglobulin receptor	11.12			
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mRNA	11.01			
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metalloproteinase 1	10.70			
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical protein	10.69			
70	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatic lipase-associated protein	10.57			
	427583	M82952	Hs.179704	NM_005588:Homo sapiens meprin, alpha (locuslink)NM_002421:Homo sapiens matrix metalloproteinase 1	10.48			
	418007	M13509	Hs.83169	NM_005819:Homo sapiens carcino-embryonic antigen	10.39			
	406741	AA058357	Hs.74486	(locuslink)NM_006890:Homo sapiens carcino-embryonic antigen	10.20			
	422424	AI186431	Hs.298638	Hs.298638:prostate differentiation factor	10.19			
	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier family 11, member 1	9.91			
75	452304	AA025385	Hs.51311	Hs.51311:ESTs, Weakly similar to S10590	9.72			
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding protein	9.70			
	430569	AF241264	Hs.178098	NM_021604:Homo sapiens angiogenesis 1	9.65			
	406687	M31128	Hs.352054	Hs.352054:pregnancy specific beta-1-glycoprotein	9.52			
80	428955	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (serum amyloid A protein)	9.47			
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX)	9.41			
	413585	AI133462	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma chain	9.39			
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens clone MCC:32871	9.31			
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGIC:22686 I	9.30			

	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cyste	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
5	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protein	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homel	8.47
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulta	8.47
	422310	AA316822	Hs.98370	{focusIn}NM_030622:Homo sapiens cytoch	8.43
10	421907	AF018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decys	8.12
	435638	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
	413881	LO0180	Hs.76599	{focusIn}NM_000488:Homo sapiens serine	7.96
	443426	AF088188	Hs.8329	{focusIn}NM_012112:Homo sapiens chrono	7.92
15	436972	AA284679	Hs.256840	Hs.25640:claudin 3	7.89
	430677	Z26317	Hs.359784	NM_01943:Homo sapiens desmoglein 2 (DSG	7.87
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cyste	7.71
	423803	NM_005709	Hs.132945	{focusIn}NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
20	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (Isof	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
	425976	C75094	Hs.334514	NM_025267:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451817	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
25	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004618:Homo sapiens transmembrane 4 s	7.12
	414617	AI339520	Hs.288817	{focusIn}NM_025130:Homo sapiens hypoth	7.10
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
	452194	AI694413	Hs.373599	Hs.373599:EST	7.02
30	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylylate cyclase	6.96
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.96
	415892	C06837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
35	414798	AI285323	Hs.97411	Hs.97411:hypothetical protein MGCI2335	6.80
	416214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411975	AI916058	Hs.144583	Hs.14583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
40	408883	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
	428970	BE276891	Hs.194691	NM_03979:Homo sapiens retinoic acid Ind	6.59
	424273	W40450	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficit	6.54
45	431330	X68532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165519	NM_031265:Homo sapiens mucin and cadher	6.50
	408243	Y00787	Hs.624	NM_000594:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056836	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
50	428753	AV939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U87058	Hs.154299	{focusIn}NM_005242:Homo sapiens coagul	6.41
	419354	M52839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032866:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AI434699	Hs.77356	Hs.77356:transient receptor (p80, CD71	6.18
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X76208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
60	426174	AA547959	Hs.115938	Hs.115938:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aktolase B, fruct	6.07
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	404953	AI885516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000876	Hs.45743	NM_000876:Homo sapiens adenosine A2b rec	6.03
65	444151	AW972917	Hs.128749	{focusIn}NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
	421408	AI680223	Hs.91096	NM_062816:Homo sapiens tripeptide motif-	5.95
	430204	AA618335	Hs.356654	Hs.356654:hypothetical protein FLJ32334	5.92
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	5.88
	408908	BE296227	Hs.250822	{focusIn}NM_003163:Homo sapiens serine	5.88
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.86
	452281	T83500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fs,	5.82
	421215	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
70	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	433083	AL042769	Hs.191762	Hs.191762:hypothetical protein MGC20298	5.75
	403218				5.75
	412104	AW205197	Hs.240951	{focusIn}NM_033120:Homo sapiens naked	5.74
	449207	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
	429345	R11141	Hs.199895	Hs.199895:hypothetical protein MAC30	5.72
75	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425208	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

408869	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67	
414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67	
413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63	
418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62	
433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apoplo	5.60	
424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-procollagen	5.59	
438746	AIB85816	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58	
414590	NM_000508	Hs.76530	NM_000508:Homo sapiens coagulation facto	5.56	
457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25-dihydroxyvitami	5.56	
10	423164	AK000232	NM_019062:Homo sapiens hypothetical prot	5.54	
409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53	
425397	J04088	Hs.156346	NM_001057:Homo sapiens topoisomerase (DN	5.53	
403221				5.52	
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 f	5.48
	418508	AW937938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 f	5.42
20	436251	BE515065	Hs.296585	(focuslink)NM_005392:Homo sapiens nucleo	5.41
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.36
	450505	NM_004572	Hs.26051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
	422535	AA311914	Hs.164578	Hs.164578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AIB47849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 f	5.32
	425334	NM_001639	Hs.1957	Hs.1957:amyloid beta component, serum	5.31
25	430580	AW138724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AI493046	Hs.148133	Hs.148133:ESTs	5.25
	419593	AA133749	Hs.301350	Hs.301350:FXYD domain-containing ion tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23856	5.21
30	415927	AL120168	Hs.78918	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83768	NM_001827:Homo sapiens CDC28 protein kin	5.20
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
35	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
	427557	NM_002659	Hs.173657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
40	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
	432575	AA553722	Hs.194346	Hs.194346:Spi-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.60758:SMC4 structural maintenance of	5.07
	427747	AW411426	Hs.180555	(focuslink)NM_004217:Homo sapiens serine	5.06
45	422609	Z46023	Hs.118721	NM_000434:Homo sapiens stardase 1 (fyo	5.06
	414361	A1086138	Hs.204044	Hs.204044:ESTs	5.04
	452340	AA028722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	436849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Dros	5.01
50	416056	BE257931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406673	M34996	Hs.198263	Hs.198263:major histocompatibility compl	4.99
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.298827	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
55	445109	AF035916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tri	4.98
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M68489	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
60	437009	AF127028	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW571178	Hs.268571	(focuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Dow syndrome critical region ge	4.91
65	414108	AI287592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422639	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW180902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
70	408162	H26530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
	434370	AF130988	Hs.58946	NM_022336:Homo sapiens ectodysplasin 1,	4.87
	413753	U17760	Hs.75517	NM_001228:Homo sapiens laminin, beta 3 (4.87
	405484				4.87
	410539	BE269047	Hs.65234	(focuslink)NM_017895:Homo sapiens DEAD/H	4.87
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
75	447343	AA256641	Hs.238894	Hs.238894:ESTs, Highly similar to S02392	4.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQG9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
	417115	AW852792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	428761	A1015709	Hs.172089	Hs.172089:pro-oncotic receptor inducing	4.78
	453751	R38762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

421943	BE616520	Hs.343912	NM_033604:Homo sapiens CAC-1 (CAC-1), mR	4.75	
400529				4.75	
407233	X16354	Hs.60964	{locuslink}NM_001712:Homo sapiens carcin	4.75	
5	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	447966	AA340605	Hs.105887	{locuslink}NM_145252:Homo sapiens simila	4.72
	439863	AW247529	Hs.6793	Hs.6793:platelet-activating factor acetyl	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	406556			4.70	
10	421506	BE302795	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
	444700	NM_003645	Hs.11728	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, rat	4.65
15	422714	AB018336	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
	403739			4.64	
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648453	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
	424825	AF207659	Hs.163357	NM_001084:Homo sapiens procollagen-lysin	4.60
20	447335	BE617695	Hs.266192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439815	Hs.76913	Hs.76913:proleasome (prosome, macrophain)	4.59
25	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
	435227	BE301871	Hs.4887	Hs.4887:mannosyl (alpha-1,3)-glycoprote	4.57
	411283	BE297802	Hs.69360	NM_006846:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:echin-A4	4.55
	409984	AW368226	Hs.57828	Hs.67928:ESTs	4.54
30	417578	AA339449	Hs.02285	NM_000819:Homo sapiens phosphoribosylgly	4.54
	432407	AA221036	Hs.1498	AF134184:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein, tyro	4.53
	403219			4.53	
35	412974	R18978	Hs.75105	NM_006579:Homo sapiens erinnopamil binding	4.52
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456905	AF117646	Hs.156637	NM_012118:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.164896	NM_000309:Homo sapiens phosphomannomutat	4.51
40	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50964	{locuslink}NM_001712:Homo sapiens carcin	4.50
	439580	AF088401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	{locuslink}NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
45	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	4.47
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422618	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW208330	Hs.356563	Hs.356563:ESTs	4.46
50	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	4.46
	442013	AA508476	Hs.376009	Hs.376009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035859	Hs.24879	Hs.24879:phosphofatty acid phosphatase t	4.45
	445417	AK001058	Hs.12880	Hs.12880:Homo sapiens cDNA FLJ10196 fts,	4.44
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
55	419559	Y7828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
	425880	L23339	Hs.1954	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW208097	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fts	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	4.43
	435777	AW419202	Hs.266192	NM_032192:Homo sapiens protein phosphata	4.42
60	422867	L23137	Hs.1584	Hs.1584:carilage oligomeric matrix prot	4.41
	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432583	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421976	AW956107	Hs.64549	{locuslink}NM_024931:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
65	412133	U38480	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422223	X84453	Hs.114366	Hs.114366:pyruvate-5-carboxylate synthe	4.38
	425998	AU076629	Hs.166950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	{locuslink}NM_017636:Homo sapiens transi	4.37
	453111	AB014688	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
70	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alpha	4.36
	429271	AF039850	Hs.198515	NM_002244:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000447	Hs.74131	NM_000447:Homo sapiens arylsulfatase E (4.34
	424865	AF011333	Hs.163563	NM_002349:Homo sapiens lymphocyte anti	4.34
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBKA_A	4.33
75	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240:Syntaxin 3A	4.32
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
80	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fts	4.29
	452017	AF109302	Hs.27485	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 f	4.29
	429638	AB916662	Hs.211577	{locuslink}NM_004986:Homo sapiens kinase	4.29

432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
443639	BE269042	Hs.9661	Hs.9661:proleosome (prosome, macropain)	4.28
418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
5	409536	AA305729	(focalink)NM_030674:Homo sapiens solute	4.27
	408989	AW361666	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530:Homo sapiens cDNA: FLJ23602	4.27
	410199	AW377424	Hs.205126:Homo sapiens cDNA: FLJ22667	4.24
10	431685	AW296135	NM_006113:Homo sapiens vav 3 oncogene [V	4.24
	409956	AW103364	NM_002192:Homo sapiens inhibin, beta A {	4.24
	413278	BE583085	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310:(focalink)NM_144624:Homo sapiens kinase	4.23
15	456629	AW891955	Hs.367942:Homo sapiens, clone IMAGE-4701	4.23
	426662	AV680038	Hs.2056:UDP glycosyltransferase 1 family	4.23
	418054	NM_002318	NM_002318:Homo sapiens lysyl oxidase-like	4.22
	418626	BE019020	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170:1hypothetical protein FLJ22969	4.21
20	435099	AC004770	NM_004111:Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078:nucleotide-sugar transporter sl	4.21
	421585	U95626	NM_0302043:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147:Homo sapiens cDNA FLJ39059	4.20
	426427	M66599	Hs.169840:TTK protein kinase	4.19
25	425283	NM_001197	NM_001197:Homo sapiens BCL2-interacting	4.19
	426031	AA295251	(focalink)NM_0063697:Homo sapiens clspa	4.19
	441085	AW136551	Hs.181245:Homo sapiens cDNA FLJ12532	4.19
	412939	AW411491	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318601	NM_021246:Homo sapiens lymphocyte antigen	4.17
30	431842	NM_005764	Hs.271473:epithelial protein up-regulate	4.17
	430387	AW372884	Hs.240770:nuclear cap binding protein su	4.17
	404826			4.17
	414198	AW505308	NM_004563:Homo sapiens phosphoenolpyruva	4.17
	434203	BE262677	Hs.283558:Homo sapiens hypothetical prot	4.17
35	426378	UR0082	Hs.166600:KIAA0826 protein	4.16
	433020	AI375728	NM_016391:Homo sapiens hypothetical prot	4.16
	420319	AW406289	NM_019034:Homo sapiens ras homolog gene	4.15
	446696	AF279265	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		NM_001746:Homo sapiens calnexin (CANX)	4.14
40	431890	X17033	Hs.271986:NM_002203:Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149:NM_014481:Homo sapiens APEX nuclease (ap	4.13
	417386	AL037222	NM_018144:Homo sapiens Sec81 alpha form	4.13
	424837	BE276113	NM_003491:Homo sapiens ARD1 homolog, N-e	4.13
	424534	D076B2	Hs.150275:KIAA0241 protein	4.13
45	445462	AAB37876	(focalink)NM_024051:Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510:Hs.184510:stratin	4.12
	409012	AL117435	Hs.49725:DKFZP434I216 protein	4.11
	424154	AF026004	NM_004366:Homo sapiens chloride channel	4.10
	400290	H18836	(focalink)NM_017636:Homo sapiens transl	4.10
50	409152	AA176585	Hs.194346:Hs.194346:Spir-2 protein	4.10
	427333	AF067797	NM_001169:Homo sapiens aquaporin B (AQP8	4.10
	413835	AI272727	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444664	N26362	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	NM_036222:Homo sapiens cytochrome P450,	4.09
55	407777	AA161071	Hs.71485:squalene epoxidase	4.09
	414806	D14694	(focalink)NM_014754:Homo sapiens phosph	4.08
	421190	U95031	Hs.102482:muclin 5, subtype B, tracheobr	4.08
	408583	RS6665	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	NM_005933:Homo sapiens nucleophosmin/nuc	4.06
60	414907	X90725	NM_009998:Homo sapiens ribosomal protein	4.06
	425247	NM_005940	Hs.155324:matrix metalloproteinase 11 (s	4.05
	443802	AW504924	Hs.9805:cexparfin 5	4.04
	411165	NM_000169	NM_000169:Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256160:NY-REN-41 antigen	4.04
65	428376	AF119665	Hs.184011:Hs.184011:pyrophosphatase (organic)	4.04
	418216	AA662240	Hs.283099:AF15q14 protein	4.02
	438278	BE396290	Hs.5097:synaptophysin 2	4.02
	421910	NM_014586	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772:collagen, type XI, alpha 1	4.02
70	449057	AAB37784	Hs.22941:KIAA1363 protein	4.01
	414561	AI084813	Hs.195165:solute carrier family 38, memb	4.00
	414812	X72755	NM_002416:Homo sapiens monokine induced	4.00
	456362	AW973003	(focalink)NM_024831:Homo sapiens nuclea	3.99
	431858	X63628	NM_001793:Homo sapiens cadherin 3, type	3.98
75	418661	NM_001949	NM_001949:Homo sapiens E2F transcription	3.98
	419092	J05581	NM_002456:Homo sapiens muclin 1, transmem	3.98
	414013	AAB76805	NM_024642:Homo sapiens hypothetical prot	3.98
	409093	BE243834	NM_015936:Homo sapiens CGI-04 protein (L	3.97
	445073	AA250970	Hs.251946:Homo sapiens cDNA FLJ11840	3.96
80	436485	X59135	Hs.156110:Hs.156110:immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398:guanine monophosphate synthetase	3.94
	449437	A1702038	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	NM_003286:Homo sapiens topoisomerase (DN	3.94

5	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent kinase 5 regulatory subunit 1B	3.94
	443180	R15875	Hs.258576	NM_012128:Homo sapiens claudin 12 (CLDN1)	3.93
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation)	3.93
	409463	A1458165	Hs.17296	NM_023930:Homo sapiens hypothetical protein	3.92
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell death 1-like protein	3.92
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, peptidase	3.91
	428658	AAB52773	Hs.334838	Hs.334838:KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fission 1	3.89
10	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanylin	3.89
	407971	A1469117	Hs.62918	Hs.62918:COC91 cell division cycle 91-II	3.89
	400750				3.89
	448140	AF146761	Hs.20480	NM_020125:Homo sapiens B lymphocyte actin	3.89
	413880	A1660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 receptor	3.89
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger protein	3.89
15	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lymphoma 10 protein	3.88
	443044	N20522	Hs.6935	NM_014298:Homo sapiens quinolinate phosphotransferase	3.88
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.88
	417129	A1381800	Hs.300684	Hs.300684:calcitonin gene-related peptide	3.87
20	410268	A216181	Hs.61635	NM_012449:Homo sapiens site transmembrane protein	3.87
	425047	U34038	Hs.154298	NM_005242:Homo sapiens coagulation factor	3.87
	416064	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidine kinase	3.86
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635:cation transmembrane epithelial protein	3.85
	407770	AW670831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1)	3.85
25	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L)	3.85
	413380	A1904232	Hs.76323	Hs.76323:prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296:ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine monophosphate) kinase	3.85
30	433858	L03678	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 like	3.84
	430237	A1272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.84
	414862	BE521310	Hs.923	Hs.923:single-stranded DNA binding protein	3.84
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens met transforming growth factor beta 1	3.84
35	427318	AF166081	Hs.175783	NM_014579:Homo sapiens solute carrier family 12 member 1	3.83
	459306	AW578452	Hs.14845	NM_0578452:RC1-CT0252-030100-023-b07 CT025	3.83
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility complex 1	3.82
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.82
40	426514	BE616633	Hs.170195	Hs.170195:bone morphogenic protein 7	3.82
	410315	A1638671	Hs.378985	Hs.378985:Homo sapiens cDNA FLJ37658 fission 1	3.82
	421905	AK660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN C03634	3.81
	421481	AW391972	Hs.104696	Hs.104696:KIAA1324 protein	3.81
	445921	AW046211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fission 1	3.80
45	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosphate kinase	3.80
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisiae homolog	3.80
	413813	M56956	Hs.75561	NM_003212:Homo sapiens tetradecanoyl acyl carrier protein acyltransferase	3.80
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mat, T-cell differentiation	3.80
	410218	T98226	Hs.171952	Hs.171952:occludin	3.80
50	407137	T97307			3.78
	430462	A1584156	Hs.105640	Hs.105640:hypothetical protein BC007772	3.78
	432680	T47364	Hs.278813	(locuslink)NM_005532:Homo sapiens Interferron regulatory factor 3	3.78
	450010	AW293801	Hs.255052	Hs.255052:ESTs	3.78
	440334	BE2761102	Hs.7165	NM_003904:Homo sapiens zinc finger protein	3.78
55	440678	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM domain 1	3.77
	428072	BE250502	Hs.182366	NM_016292:Homo sapiens heat shock protein	3.77
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyridoxamine) kinase	3.77
	428459	A151812	Hs.168992	NM_015966:Homo sapiens serologically defined	3.77
	443323	BE660621	Hs.9222	Hs.9222:estrogen receptor binding site a	3.76
60	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.76
	423198	M81933	Hs.16134	Hs.16134:cell division cycle 25A	3.76
	428205	AB020643	Hs.163006	Hs.163006:likely homolog of mouse heparanase	3.75
	447200	BE543148	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fission 1	3.74
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens caspase kinase 2, S. cerevisiae homolog	3.74
65	411950	T28407	Hs.81664	NM_002619:Homo sapiens platelet factor 4	3.74
	418661	AA287785	Hs.23449	Hs.23449:insulin receptor tyrosine kinase	3.74
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical protein	3.74
	446291	BE397753	Hs.146233	Hs.146233:interferon, gamma-inducible protein 39	3.74
	435836	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular carcinoma-associated protein	3.73
70	417286	AA222337	Hs.81874	NM_002413:Homo sapiens microsomal glutathione reductase	3.73
	421743	T35958	Hs.107614	Hs.107614:DXFZP564117 protein	3.73
	400419	AF084645		AF084645:Homo sapiens versican Vnt Isoform	3.73
	421357	AK000809	Hs.103808	NM_017895:Homo sapiens chromosome 20 open reading frame	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
75	418703	NM_014448	Hs.87435	Hs.87435:rRNA guanine exchange factor (GE)	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transmembrane protein	3.72
	419743	AW409762	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA sequence	3.72
	436730	AB020535	Hs.4984	Hs.4984:KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.72
80	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypothetical protein	3.72
	442875	BE623003	Hs.23626	Hs.23626:Homo sapiens clone TCCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjugating enzyme E2L	3.71
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fission 1	3.71
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypeptide	3.71

	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++/iron	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
5	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
	408486				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AI594131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
	416650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
10	413179	N95692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenase	3.69
	428543	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
15	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibitor, beta C (3.69
	442315	AA173992	Hs.7956	Hs.7956:E81s	3.68
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA305007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
20	418558	AW082266	Hs.86131	Hs.88131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-raf simian leuk	3.66
	409402	AF208234	Hs.695	Hs.695:Cystatin B (stefin B)	3.66
	436014	AF281134	Hs.263741	NM_020168:Homo sapiens exosome component	3.66
25	432633	AJ763390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248287	(locuslink)NM_021126:Homo sapiens mercap	3.66
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	437020	UB5768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432920	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
30	420185	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA120265	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI807114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165863	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
35	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
	452098	AI858183		BF755039:QV0-CT0583-181000-428-107 CT058	3.62
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.35844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
40	400847				3.60
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
45	453331	AI240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31066 f1s	3.60
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
	417369	BE260904	Hs.82045	Hs.82045:mikihime (neutrophil growth-promoti	3.59
	419507	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
50	446356	AI816738	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001660:Homo sapiens Interleukin 13 re	3.59
	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420631	A1652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
55	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AI41332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
	424241	AW95948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, 1	3.57
	452284	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AI110291	Hs.99364	Hs.99364:hydrolase domain containing 1	3.56
	434224	AA380731	Hs.84	NM_000206:Homo sapiens Interleukin 2 rec	3.56
60	425322	U83630	Hs.155537	NM_005904:Homo sapiens protein kinase, D	3.56
	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initia	3.56
	413859	AWS92355	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, 1	3.56
	427288	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
	436127	W948324	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
	411704	AI499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
	452700	AI859390	Hs.288940	NM_021269:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyl a	3.54
	453323	AF034102	Hs.32551	NM_001532:Homo sapiens solute carrier fa	3.54
65	422813	AV858571	Hs.121088	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs Moderately similar to S1	3.54
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transm	3.53
	421802	BE281458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
70	428582	BE336899	Hs.185055	Hs.185055:BENP protein	3.53
	446147	AL133064	Hs.14051	(locuslink)NM_145658:Homo sapiens endoza	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.52
	442007	AA301118	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
75	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens ED6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens culin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
442993	BE018692	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
404240				3.50
5	424909	S78187	Hs.153752 (focuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AA452943	(focuslink)NM_003779:Homo sapiens UDP-Ga	3.49
	424954	NM_000546	NM_000546:Homo sapiens tumor protein p63	3.49
10	424142	AI678727	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	U52112	Hs.182018:interleukin-1 receptor-associa	3.49
	456534	X31195	NM_106223:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	NM_002219:Homo sapiens integral membrane	3.49
15	439841	AF038951	NM_004870:Homo sapiens mannose-P-dolicho	3.49
	428390	AI640377	NM_000982:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	NM_017423:Homo sapiens UDP-N-acetyl-alpha	3.48
	431183	NM_006885	NM_006885:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE3387202	Hs.118838:Hs.118838:non-metastatic cells 1, prote	3.48
20	457635	AV660976	Hs.3569:chromosome 20 open reading frame	3.48
	419705	AW366634	Hs.154331:ESTs	3.48
	454390	AB020713	(focuslink)NM_024923:Homo sapiens hypoth	3.48
	402629			3.47
	451707	AW051061	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433804	NM_013442	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AI741809	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA756142	Hs.131810:Homo sapiens cDNA FLJ36976 fis	3.47
	439223	AW238299	NM_026217:Homo sapiens UL16 binding prot	3.46
	452203	X57522	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW296454	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	Hs.9799	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	(focuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AI359575	Hs.23765:membrane metallo-endopeptidase	3.45
	427581	NM_014788	NM_014788:Homo sapiens tripartite motif	3.45
35	436327	AF078866	Hs.284296 NM_03161:Homo sapiens surfel 4 (SURF4)	3.45
	400263		NM_001961:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007:Homo sapiens, Similar to LOC16	3.45
	410836	AA088177	Hs.172870:KIAA1913 protein	3.45
	456850	AF111120	Hs.306165:ESTs, Highly similar to unknown	3.44
40	432391	AI732374	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA352104	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	NM_001669:Homo sapiens arylsulphatase D {	3.44
	425274	BE281181	NM_155462:MCM6 minichromosome maintenanc	3.44
45	448913	AA194422	NM_049992:Homo sapiens myosin VI (MYO6).	3.44
	448847	AI587180	Hs.110906:hypothetical protein BC004501	3.44
	420163	AW732276	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	NM_001200:Homo sapiens bone morphogeneti	3.43
	424482	BE268621	(focuslink)NM_003374:Homo sapiens voltage	3.43
50	414198	U33446	Hs.75799:protease, serine, 8 (prostasin)	3.43
	422296	W21872	(focuslink)NM_145059:Homo sapiens L-fuco	3.43
	426093	AW584506	Hs.104830 Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183556:solute carrier family 1 (neur	3.42
	445580	AF167572	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
55	442821	BE391929	Hs.8752:transmembrane protein 4	3.42
	427597	D16849	NM_028442:Homo sapiens protein tyrosine	3.42
	427648	AI376722	Hs.180062:proteasome (prosome, macrophain	3.41
	428734	BS303044	NM_03767:Homo sapiens eukaryotic transl	3.41
	453802	BE502341	NM_139177:Homo sapiens chromosome 17 ope	3.41
60	441565	AW953575	Hs.303125:Hs.303125:cpx53-induced protein PIGPC1	3.41
	414045	NM_002951	NM_002951:Homo sapiens ribophorm II (RP	3.41
	423323	AI951628	NM_003740:Homo sapiens potassium channel	3.41
	443303	U87319	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	NM_033576:Homo sapiens serine/threonine	3.40
65	422256	M64673	NM_005526:Homo sapiens heat shock transci	3.40
	451129	BE072881	BE072881:RC2-BT0548-201300-012-e09 BT054	3.40
	402025		NM_006266:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	NM_004182:Homo sapiens ubiquitinously-expr	3.39
	417457	AA378907	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363			3.39
	444758	AL044878	NM_000859:Homo sapiens 3-hydroxy-3-methyl	3.39
	423309	BE006776	NM_014467:Homo sapiens sushi-repeat prot	3.38
75	426125	X87241	Hs.185994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119666	NM_018842:Homo sapiens insulin receptor	3.38
	400125		(focuslink)NM_004162:Homo sapiens ornith	3.38
80	429404	NM_005738	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	NM_018992:Homo sapiens hypothetical prot	3.37
	434628	AF155661	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI805664	(focuslink)NM_012094:Homo sapiens peroxi	3.37
	427715	BE245274	Hs.180428:kAAA1181 protein	3.37

	446715	AJ337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SW/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
	406698	X03088	Hs.73931	Hs.73931:major histocompatibility comple	3.36
5	439778	AL109729	Hs.99384	Hs.99384:albhydrolase domain containing 1	3.36
	418882	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.35
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.35
	436415	BE285264	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
15	457329	AI634860	Hs.359582	(locuslink)NM_016442:Homo sapiens type 1	3.35
	432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphatidyly	3.35
	412625	AA581439	Hs.162328	Hs.162328:ESTs	3.35
	416391	AB78927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D22643	Hs.34789	NM_005218:Homo sapiens dolichyl-diphosph	3.35
20	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
	400262	BE247600	Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens apelin-B1 (EFNB1)	3.34
	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
25	437295	AA350394	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carboxyl-phospha	3.34
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finksi	3.34
	439246	AI498072	Hs.361474	Hs.361474:Homo sapiens cDNA FLJ30002 fis	3.34
30	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
	446350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208812	Hs.208912:hypothetical protein MGCB61	3.33
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
35	415938	BE388307	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.75871	(locuslink)NM_012408:Homo sapiens protel	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AJ574985	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW9568941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	3.32
	430393	BE185030	Hs.241305	(locuslink)NM_005470:Homo sapiens tripar	3.32
45	402104				3.32
	446620	AA128808	Hs.178902	(locuslink)NM_022109:Homo sapiens CDwB2	3.32
	443425	AJ056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926980	Hs.348669	Hs.348669:CDC28 protein kinase 1	3.31
	413063	AL03737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage 9	3.31
	451564	AU078693	Hs.132780	(locuslink)NM_001467:Homo sapiens glucos	3.31
50	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
	441886	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343281	Hs.343281:histocompatibility (minor) 13	3.31
	422192	AA305159	Hs.113019	NM_016331:Homo sapiens fts485 (LOC51086)	3.31
	446606	AJ123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cytoso	3.31
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.31
	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
55	428157	AT38719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018896:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sera domain, immu	3.30
65	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.29
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
	442772	AW903680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI678842	Hs.237924	NM_016016:Homo sapiens CG-69 protein (L	3.29
	446163	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
70	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cyste	3.29
	417891	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
	412926	AI879078	Hs.75061	Hs.75061:macrophage myristoylated alanyl	3.28
	427308	D26057	Hs.174805	Hs.174905:KIAA0033 protein	3.28
	432026	AA624545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
	449199	AI880122	Hs.196988	Hs.196988:ESTs	3.28
75	442739	NM_007274	Hs.38679	(locuslink)NM_007274:Homo sapiens cytoso	3.28
	422051	AW327546	Hs.111024	(locuslink)NM_0D5984:Homo sapiens solute	3.28
	452714	AW770894	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
	431884	AA521246	Hs.210792	He.210792:Homo sapiens cDNA FLJ36691 fis	3.28
80	402260				3.27
	408666	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens mafid	3.28
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
	426812	AF105365	Hs.172813	NM_005593:Homo sapiens solute carrier fa	3.27

429571	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27	
434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (Importin al	3.27	
454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27	
445093	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27	
5	448752	AA593867	NM_024829:Homo sapiens KIAA1608 protein	3.26	
425221	AV649864	Hs.155188	NM_005842:Homo sapiens TAF7 RNA polymerase	3.26	
440286	U29589	Hs.7138	NM_00740:Homo sapiens cholinergic recep	3.26	
413745	AW247252	Hs.75514	NM_00270:Homo sapiens nucleoside phosph	3.26	
10	412338	AA151527	(focuslink)NM_024661:Homo sapiens hypoth	3.26	
426520	BE545884	Hs.343668	Hs.343668;KIAA0251 protein	3.26	
427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26	
440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26	
425866	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25	
15	416448	L13210	NM_005567:Homo sapiens lectin, galactosi	3.25	
449944	AF290512	Hs.58215	(focuslink)NM_033046:Homo sapiens rholet	3.25	
424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25	
425784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25	
420190	AI816208	Hs.95867	(focuslink)NM_024112:Homo sapiens chromo	3.25	
20	438085	RS2518	Hs.7967	Hs.7967:ESTs, Weakly similar to extenin	3.24
419216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24	
430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24	
458376	AB023179	Hs.9059	Hs.9059;KIAA0962 protein	3.24	
410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24	
25	420676	AI434780	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24	
435640	AF220053	Hs.54950	NM_018468:Homo sapiens uncharacterized h	3.23	
427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23	
412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23	
430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23	
30	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23	
410340	AW182833	Hs.112188	(focuslink)NM_021826:Homo sapiens hypoth	3.23	
410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23	
430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23	
35	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
438075	BE090176	Hs.179902	NM_080546:Homo sapiens Cdw92 antigen (CD	3.22	
403912				3.22	
429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22	
416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22	
445229	AB028013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22	
422030	X51416	Hs.110849	(focuslink)NM_004451:Homo sapiens estrog	3.22	
409691	AA532963	Hs.9100	Hs.8100:hypothetical gene supported by A	3.22	
411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22	
414820	AA371931	Hs.77422	Hs.77422:proteinlipid protein 2 (colonic	3.22	
450770	AA015924	Hs.28803	Hs.28803:ESTs	3.22	
45	433223	AB040927	Hs.301804	Hs.301804;KIAA1494 protein	3.22
414172	AW854324	Hs.75790	(focuslink)NM_002942:Homo sapiens phosph	3.21	
428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21	
432078	BE314877	Hs.24553	(focuslink)NM_022369:Homo sapiens hypoth	3.21	
50	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21	
409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21	
400836				3.20	
55	420261	AI623693	Hs.323494	(focuslink)NM_017984:Homo sapiens hypoth	3.20
414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20	
447086	BE539189	Hs.62112	(focuslink)NM_003457:Homo sapiens zinc f	3.20	
412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20	
426281	BE385099	Hs.356814	Hs.356814:Homo sapiens clone IMAGE:28333	3.20	
407738	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30577 fis	3.20	
60	400845			3.20	
407082	Z47055			3.20	
452012	AA307703	Hs.279766	(focuslink)NM_012310:Homo sapiens kinesi	3.20	
403217				3.20	
414249	AI797994	Hs.279929	(focuslink)NM_017510:Homo sapiens gp25L2	3.19	
431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphil	3.19	
417777	AB23763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19	
457274	AW574193	Hs.227152	NM_016381:Homo sapiens hypothetical prot	3.19	
445139	AB037849	Hs.12365	Hs.12365:synaptotagmin XIII	3.19	
430260	AA351258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19	
70	422197	AW974265	Hs.111632	Hs.111632:Lem3 protein	3.19
422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere prot	3.18	
435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18	
449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18	
426925	NM_001196	Hs.172894	Hs.172894:BH3 interacting domain death a	3.18	
75	414814	D14897	Hs.77393	(focuslink)NM_002004:Homo sapiens farnes	3.18
405387				3.18	
444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18	
424089	AL036652	Hs.144949	Hs.144949:ESTs	3.17	
414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17	
424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D24	3.17	
80	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17	
447032	AK000310	Hs.17138	(focuslink)NM_017755:Homo sapiens hypoth	3.17	
410563	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17	

			Hs.177576:mannosyl (alpha-1,3)-glycopro	3.17	
415402	AA164687	Hs.177576	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17	
451032	W03692	Hs.323079	Hs.73722:APEX nuclease (multifunctional	3.17	
412146	M92444	Hs.73722	Hs.80887:y-yes-1 Yamaguchi sarcoma viral	3.16	
417018	M16038	Hs.80887	NM_022105:Homo sapiens death associated	3.16	
5	425244	AK002127	Hs.155313	Hs.62845:Homo sapiens cDNA: FLJ21930 fts	3.16
	417878	I9J0916	Hs.82845	Ha.13122:hypothetical protein FLJ14524	3.16
	426675	AW084791	Hs.133122	NM_006979:Homo sapiens HLA class II regl	3.16
	432728	NM_006979	Hs.278721	{locuslink}NM_004697:Homo sapiens PRP4 p	3.16
10	442643	U82758	Hs.374973	Hs.85265:integrin, beta 4	3.16
	418462	BE001596	Hs.85266	NM_005318:Homo sapiens H1 histone family	3.16
	429922	Z97630	Hs.226117	Hs.314807:hypothetical protein MGCG2655	3.16
	429556	AW135939	Hs.314807	{locuslink}NM_002380:Homo sapiens membra	3.15
	418127	BE243982	Hs.83532	Hs.79162:structure specific recognition	3.15
15	416293	BE244454	Hs.79162	NM_030926:Homo sapiens Integr	3.15
	435968	AW161481	Hs.111577	NM_004359:Homo sapiens cell division cyc	3.15
	414702	L22005	Hs.76932	NM_016230:Homo sapiens flavohemoprotein	3.15
	437672	AW748265	Hs.5741	Hs.4990:KIAA1089 protein	3.14
	435750	AB029012	Hs.4990	NM_005898:Homo sapiens membrane componen	3.14
20	432710	AA609685	Hs.278572	NM_005898:Homo sapiens membrane complex	3.14
	407961	AW872939	Hs.41694	Ha.41694:origin recognition complex, sub	3.14
	438203	BE540000	Hs.7345	He.7345:MAD1 mitotic arrest deficient-II	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	{locuslink}NM_003661:Homo sapiens apolip	3.14
25	450285	T1768732	Hs.210528	Ha.210628:ESTs	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780199	Hs.30327	NM_036668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW541818	Hs.290216	Hs.290216:ESTs	3.13
30	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (transf	3.13
	447627	AF080922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Ha.94761:KIAA1691 protein	3.12
35	438444	AI054707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	424727	AW5910378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fts	3.12
	436975	AL118990	Hs.373554	{locuslink}NM_130786:Homo sapiens alpha-	3.12
	426680	BE161811	Hs.171811	NM_001625:Homo sapiens adenylyl kinase	3.12
	412326	R07586	Hs.73817	NM_022983:Homo sapiens small inducible c	3.12
40	409220	BE243323	Hs.51233	{locuslink}NM_003842:Homo sapiens tumor	3.12
	428599	AW578252	Hs.190161	Hs.190161:LR8 protein	3.12
	422675	BE018517	Hs.119140	NM_001870:Homo sapiens eukaryotic transl	3.12
	444301	AK000138	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI375750	Hs.57600	NM_001283:Homo sapiens adapt7-related p	3.12
45	419152	L12711	Hs.89643	{locuslink}NM_001054:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptobatin 2	3.12
	413073	ALD38165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	405865	AI025931	Hs.181357	Hs.181357:lectin receptor 1 (67kD, fibo	3.11
	405203				3.11
50	441028	AI339660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	428824	AA295363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fts	3.11
	426234	BE314534	Hs.166169	Hs.166169:binational apoptosis regulat	3.11
55	408805	H69912	Hs.48269	NM_003384:Homo sapiens vacuola related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	416976	AI243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:zinc-nestin homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:claudin-9 and nestin/cytokeratin	3.10
60	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 f	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	A1278002	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_008516:Homo sapiens solute carrier fa	3.10
	435472	AW972390	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	3.10
	436906	H95390	Hs.181244	Hs.181244:major histocompatibility compl	3.10
70	427337	Z46223	Hs.176663	NM_005693:Homo sapiens Fc fragment of Ig	3.10
	433495	BE545277	Hs.940859	NM_005725:Homo sapiens Ts translation el	3.09
	408150	BE520274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-8	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
75	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens fibrophorin I (RPN	3.09
	449051	AW981400	Hs.33326	NM_032339:Homo sapiens hypothetical prot	3.09
	426297	AA236291	Hs.183683	NM_030565:Homo sapiens serine (or cyste	3.09
	430066	AI929559	Hs.237825	Hs.237825:signal recognition particle 72	3.09
80	428044	AA093322	Hs.301404	NM_005743:Homo sapiens RNA binding motif	3.09
	426989	A1815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine {	3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fts	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	3.08

	410668	BE378794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U66839	Hs.180533	NM_002758:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisP	3.08
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl amidopeptidase	3.07
10	411423	AW845987	Hs.68864	(focuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to cholinesterase	3.07
	448719	AA033627	Hs.21658	Hs.21658:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicrobial peptide	3.07
15	450876	AF189062	Hs.285976	(focuslink)NM_013384:Homo sapiens LAG1	3.07
	432465	D56165	Hs.275163	NM_032612:Homo sapiens non-metastatic ce	3.07
	421808	AIK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	HW59354	Hs.374303	(focuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.06
20	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418062	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (3.06
	407223	H56850		Hs.95650;yw03b12.81 Soares melanocytla 2NbH	3.06
	418841	BE243135	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
25	450690	AA296898	Hs.333418	(focuslink)NM_014164:Homo sapiens FXYD d	3.06
	408124	UR9337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
	435550	AI224458	Hs.324507	Hs.324507:hypothetical protein FLJ20988	3.06
	421779	AI879159	Hs.108219	NM_004628:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	445770	AV660309	Hs.164986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038952	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412867	AI076881	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA475866	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.45328	Hs.45328:fucosyltransferase 2 (secretor)	3.05
	408102	U46351	Hs.621	Hs.621:lectin galactoside-binding, solu	3.05
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
40	432261	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA4714212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AWB363036	Hs.128819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
45	447436	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
	453450	AWT97627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
50	412708	R26830	Hs.108137	Hs.108137:Homo sapiens mRNA for CK/SW-CL	3.04
	448569	BE582657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.256838	NM_031457:Homo sapiens membrane-spanning	3.03
	412527	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	443039	U83236	Hs.10803	Hs.10803:calcium and Integrin binding 1	3.03
55	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430354	AA854810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184288	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 284	3.02
	417888	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, facili	3.02
	418741	H83265	Hs.8861	Hs.8861:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355128	(focuslink)NM_144686:Homo sapiens hypoth	3.01
	424867	AI024880	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022494:Homo sapiens hypothetical prot	3.01
	437651	BE560672	Hs.13543	(focuslink)NM_145214:Homo sapiens triplex	3.01
70	436540	BE397032	Hs.14468	NM_020280:Homo sapiens pterin pan homolog	3.00
	438000	AI825880	Hs.5985	Hs.5985:non-kinesin Cdc42 effector prot	3.00
	415697	AI365603	Hs.279896	Hs.279896:DXFZP56511024 protein	3.00
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
75	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
	450126	BE018138	Hs.24447	(focuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE521800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406868	AA505445	Hs.300697	Hs.300697:immunglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
80	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related ante	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	406685	Q_0	M18728
10	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847619 AA099425 AW817981 AW856386 BG961122 AA224498 AA308542 AW821833 BF902156 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748364 BF739224 BG961655 AK067283 BI881466 AA663341 AA457591 BG949294 AW392866 AA071122 AA227849 AA684918 BG959570 BF773486 ALD04698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF004964 AW818172 AW818143 AW392930 AW817057 AW858044 BF745211 AA170928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055692
15	459306	223120_4	AW578452
	452098	161393_1	BG028348 BF772844 HB3065 AW817969 H90985 BF755039 AI858183
	451129	1495811_1	BE072881 AI762181 BE072946

TABLE 11C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., *Nature* (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	406399	9256288	Minus	63448-63564
30	403220	7630969	Plus	6433B-64517
	403218	7630969	Plus	58039-58149
	403221	7630989	Plus	65294-68438,68936-67124
	405484	5922026	Plus	199214-199579,199672-199920,200262-20049
	400529	9795988	Plus	138232-138423
35	405556	1552611	Plus	153497-163623,164715-164968,165369-16550
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630869	Plus	61858-61955
	404628	6572184	Plus	47728-48046
	400750	8119067	Plus	198991-199168,199316-199548
40	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
45	404240	5002624	Minus	116132-116407,116653-116922
	402829	8918414	Plus	101532-101852,102006-102263
	408363	9256114	Plus	14403-14602,17000-17147,17241-17368
	402104	8119072	Plus	122409-122500
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
50	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	400836	8954179	Plus	677-1188
	400845	9168605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6587915	Minus	3769-3833,5708-5895
55	405203	7230116	Plus	125295-125463

Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59880 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93rd percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93rd percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

65 TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
75	402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	38.9
	435094	AI560129	Hs.329062	EST	30.3
	439606	W79123	Hs.68561	G protein-coupled receptor 87	28.8
80	452240	AI591147	Hs.61232	ESTs	27.0
	444783	AK001468	Hs.62180	anillin (<i>Drosophila</i> Scraps homolog), actin binding protein	26.0
	417034	NM_006183	Hs.80962	neurotansin	25.5
	424046	AF027886	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

	435505	AF200492	Hs.211238	interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine protease inhibitor 13 (P113; serpin	20.1
	452461	N78223	Hs.108105	transcription factor	19.8
5	423017	AW178761	Hs.227946	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptosomal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292866	Hs.251373	hypothetical protein J434014.3	16.3
	428664	AK001698	Hs.189095	similar to SALL1 (sal (<i>Drosophila</i>)-like	16.2
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA235776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens cgs5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.125911	ESTs	13.4
	417366	BE185288	Hs.1076	small proline-rich protein 1B (comifin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
	404956			Target Exon	13.1
20	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013867	Hs.72047	ESTs*	12.9
	428618	AA885260	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
25	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
	429466	AF155927	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31162	Hs.179729	collagen, type X, alpha 1 (Schmid metapheal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cysteatein associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423048	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
	439926	AW014875	Hs.137007	ESTs	10.2
40	428388	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homo box A13	10.2
	442650	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055611	Hs.226588	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.293853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057	NM_007057	NM_007057* Homo sapiens ZW10 interactor (ZW10	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AW420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455601	AI368880	Hs.816	BRY (sex determining region Y)-box 2	9.4
	418882	NM_004993	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437769	AI561344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.B9764	fragile X mental retardation 1	9.1
55	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	9.1
	420502	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153810	KIAA0751 gene product	9.0
	428427	MB6899	Hs.168840	TTK protein kinase	9.0
	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
60	446232	AI281848	Hs.194681	retinoic acid induced 3	8.9
	430520	NM_016190	NM_242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10258	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	A383032	Hs.1608	replication protein A3 (14kD)	8.9
65	430486	BE062109	Hs.241551	chloride channel, calcium activated, family m	8.7
	452291	AF016592	Hs.28853	CDC7 (cell division cycle 7, <i>S. cerevisiae</i> , h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963	gb:MR0-ST0032-200899-001-b11-ST0032	Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
70	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
	424086	AJ351010	Hs.102257	trypt oxidase	8.3
	420092	AAB14043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:hs41a09,x1 NCL_CGAP_Ut1 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human, odont	8.2
	418478	U3B945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
75	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
	410044	BE568742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
80	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Bauren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA668879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
	406654			Target Exon	7.4
5	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86617	ESTs	7.2
	446364	AB008824	Hs.14912	KIAA0286 protein	7.2
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast)	7.1
10	414148	BE084049	gb:PM0-BT0651-270400-003-f02 BT0651 Homo sapi		7.0
	428548	AW138872	Hs.135288	ESTs	7.0
	423725	AI403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24598	RAD51-interacting protein	7.0
	450149	AW989781	Hs.132663	Zic family member 2 (odd-paired Drosophila ho	6.9
15	319141	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.195729	ESTs	6.9
20	450028	AI912012	Hs.200737	ESTs	6.8
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10687	similar to lysosome-associated membrane glyco	6.8
	413573	AI733889	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
	454988	AWB80140	gb:IL3-CTD219-281099-023-D11 CT0219 Homo sapi		6.8
25	447342	A1199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	405041	AB033025	Hs.50081	KIAA1198 protein	6.7
	407839	AA045144	Hs.161586	ESTs	6.6
30	415652	T79213	Hs.272073	ESTs	6.6
	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	446693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
35	436622	AW979271	Hs.293184	ESTs	6.5
	457405	AA504860	gb:ab03a10.s1 Stratagene fetal retina 937202		6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT2RP20	6.4
	414812	X72755	Hs.77367	monokine induced by gamma Interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monoxygenase	6.3
40	446435	AW205737	Hs.253582	ESTs	6.3
	421948	L42583	Hs.334309	keratin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12088	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	AI925153	Hs.217493	annexin A2	6.2
45	453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
	423735	AA330259	gb:EST33963 Embryo, 12 week II Homo sapiens c		6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142853	ret finger protein	6.1
50	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fs, clone HEMBB10	6.1
	427043	AA397679	Hs.3991	ESTs	6.1
	409723	AW885757	Hs.257662	ESTs	6.1
	459462	AA481396	Hs.105167	ESTs	6.1
	423244	AL039379	Hs.209802	ESTs, Weakly similar to ubiquitously TPR motif,	6.0
	427217	AA399272	Hs.144341	ESTs	6.0
55	441820	AA989119	Hs.143602	ESTs, Weakly similar to envelope protein β -Ls	6.0
	437858	BE139560	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA468293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	HB1219	Hs.148225	ESTs, Weakly similar to KIAA1503 protein [H.s	5.9
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.9
60	434828	D90070	Hs.96	photol-12-myristate-13-acetate-induced prote	5.9
	414299	AA142989	Hs.71730	ESTs	5.8
	439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	ferritin, beta 3 (nicsin (125kD), kathrin (140	5.8
	413825	AW451103	Hs.71371	ESTs	5.8
	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
	415054	AA159804	Hs.149305	hypothetical protein MGC2803	5.7
	425695	NM_006401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	416900	Z43758	Hs.28037	ESTs	5.7
65	444747	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	449611	AI970394	Hs.197075	ESTs	5.7
	420637	AW976153	gb:EST388262 MAGE resequences, MAGN Homo sapi		5.7
	438039	AI278360	Hs.31409	ESTs	5.7
	414972	BE263702	Hs.77695	KIAA0008 gene product	5.7
75	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
	428365	AA295331	Hs.163861	Homo sapiens cDNA FLJ20042 fs, clone COL0042	5.6
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2933	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW293207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41690	desmocollin 3	5.5
	410859	AI080175	Hs.68826	ESTs	5.5
	432869	AW974094	gb:EST386197 MAGE resequences, MAGM Homo sapi		5.5

431255	AA497043	Hs.115685	ESTs	5.5
407366	AF026942		gb:Hom sapiens cig33 mRNA, partial sequence.	5.5
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
418502	R99288	Hs.35152	ESTs	5.4
5	440320	AA879294	gb:Hom sapiens s1 NCI_CGAP_Pr12 Homo sapiens cDNA	5.4
	439679	AF086400	gb:Hom sapiens full length insert cDNA clone	5.4
	420783	AI659838	Hs.99923 lectin, galactoside-binding, soluble, 7 (gal-	5.4
	408536	AW381632	ESTs	5.4
	408756	NM_003686	exonuclease 1	5.4
10	451411	AA017492	Hs.135655 EST	5.4
	424834	AK001432	Hs.153408 Homo sapiens cDNA FLJ10570 fs, clone NT2RP20	5.3
	407853	AA336797	Hs.404999 dickkopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625 RAB6 interacting, kinesin-like (rabkinesin 6)	5.2
	420026	AI831190	Hs.166676 ESTs	5.2
15	427356	AW023482	Hs.97849 ESTs	5.2
	420440	NM_002407	Hs.97644 gammaglobin 2	5.2
	430082	AW514083	Hs.190135 ESTs	5.2
	445259	AI798994	Hs.152923 ESTs	5.2
	457345	AI699933	Hs.192175 ESTs	5.2
20	453161	A6628608	Hs.61655 ESTs	5.2
	445019	AI205540	Hs.281295 ESTs	5.2
	425420	BE536911	Hs.234545 hypothetical protein NUF2R	5.2
	439706	AW072527	Hs.59761 ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
	431484	AA991355	Hs.298312 hypothetical protein DKFZp434A1315	5.2
25	443179	AB28402	Hs.6933 hypothetical protein FLJ12684	5.2
	432228	AW182766	Hs.273558 phosphate cytidyltransferase 1, choline, al	5.2
	441020	W79283	Hs.35962 ESTs	5.1
	437044	AL035864	Hs.69517 cDNA for differentially expressed CO16 gene	5.1
	419520	AB009303	Hs.90800 matrix metalloproteinase 16 (membrane-inserte	5.1
30	430563	AA481269	Hs.108660 ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547		NM_018833;Homo sapiens transporter 2, ATP-bi	5.1
	435206	AI432364	Hs.160594 ESTs	5.1
	409289	AI576953	Hs.22972 hypothetical protein FLJ13352	5.1
	439223	AW238299	Hs.250618 UL16 binding protein 2	5.1
35	413261	AI932903	Hs.211595 ESTs	5.1
	426320	W47695	Hs.169300 transforming growth factor, beta 2	5.1
	458829	AI557388	Hs.6682 gbPT2.1_6_G03.r tumor2 Homo sapiens cDNA 3'	5.0
	416208	AW291168	Hs.41295 ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
	432473	AI202703	Hs.152414 ESTs	5.0
40	418736	AW588633	Hs.66862 solute carrier family 7, (cationic amino acid	5.0
	423634	AW959908	Hs.1690 heparin-binding growth factor binding protein	5.0
	428350	NM_003245	Hs.2022 transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016836	Hs.233364 ESTs	5.0
	449448	D60730	Hs.57471 ESTs	5.0
45	409744	AW875258	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
	405657		C7000246;gl[72477 pri]DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602 SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI37228	ESTs	4.9
	434376	AA631492	Hs.23921 hypothetical protein DKFZp547A023	4.9
50	407378	AA299264	Hs.57776 ESTs, Moderately similar to I38022, hypothetical	4.9
	421155	H87879	Hs.102267 lysyl oxidase	4.9
	443335	T88897	Hs.16845 ESTs	4.9
	444461	R53734	Hs.25978 ESTs, Weakly similar to 2109260A B cell growt	4.8
	410361	BE391804	Hs.62661 guanylate binding protein 1, Interferon-induc	4.8
55	423673	BE003054	Hs.16985 matrix metalloproteinase 12 (macrophage elast	4.8
	441720	A346487	Hs.28739 ESTs	4.8
	442980	AA857025	Hs.8978 kinesin-like 1	4.8
	450375	AA008647	Hs.8650 a disintegrin and metalloproteinase domain 12	4.8
	417592	AA204664	Hs.182437 ESTs, Weakly similar to 154383 chromosome seg	4.8
60	429846	AB023021	Hs.225945 fucosyltransferase 9 (alpha (1,3) fucosytran	4.8
	418399	AW630803	Hs.89497 lamin B1	4.7
	417235	AA810278	Hs.24250 ESTs	4.7
	419158	AA099020	gb:zv45h01.s1 Stratagene HeLa cell s3 937216	4.7
	433658	N68243	Hs.192974 hypothetical protein FLJ12795	4.7
65	450434	AA168950	Hs.195870 hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516 filgotin-like 1	4.7
	401747		Homo sapiens keratin 17 (KRT17)	4.7
	439758	AL359055	Hs.67709 Homo sapiens mRNA full length insert cDNA clo	4.7
	441421	AA356792	Hs.334824 hypothetical protein FLJ14825	4.7
70	457465	AW301344	Hs.122908 DNA replication factor	4.6
	433159	AB036998	Hs.150587 kinesin-like protein 2	4.6
	412333	AW937485	gb:QV3-DT0044-221299-045-b03 DT0044 Homo sapi	4.6
	401137		Target_Exon	4.6
	401575		Target_Exon	4.6
75	423448	AK000776	Hs.128763 Homo sapiens cDNA FLJ20769 fs, clone COLO667	4.6
	421978	AJ243662	Hs.110195 NCSE-1 protein	4.6
	408728	AL137379	Hs.47125 hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245 Homo sapiens cDNA FLJ11170 fs, clone PLACE10	4.6
	450510	AA010056	Hs.242998 ESTs	4.6
80	436291	BE568452	Hs.5101 protein regulator of cytokinesis 1	4.6
	424902	NM_003886	Hs.153687 inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601 solute carrier family 7 (cationic amino acid	4.5
	449416	AI851016	Hs.246311 ESTs	4.5

416168	H23687		gb:yn72d12_r1 Soares adult brain N2b6HB55Y Ho	4.5	
447033	AI357412	Hs.157601	ESTs	4.5	
446353	AI290919	Hs.153681	ESTs	4.5	
443715	AI583187	Hs.9700	cyclin E1	4.5	
5	454707	AIW14989	gb:MR1-ST0206-170400-024-q05 ST0206 Homo sapi	4.5	
	438435	TB9473	Hs.192328	ESTs	4.5
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	4.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	4.4
10	422809	AK001379	Hs.121029	hypothetical protein FLJ10549	4.4
	430919	AA489041	Hs.295448	ESTs	4.4
	435313	AI765400	Hs.189729	ESTs	4.4
	425071	NM_013989	Hs.154424	diodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	ESTs, Weakly similar to I38022 hypothetical p	4.4
15	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (p150)	4.4
	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.4
	444781	NM_0014400	Hs.11950	GPI-anchored metastasis-associated protein ho	4.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.4
	414035	Y0063D	Hs.75716	serine (or cysteine) proteinase inhibitor, cl	4.4
20	416216	AA682240	Hs.283099	AF4sq14 protein	4.4
	446252	AI283125	Hs.150009	ESTs	4.4
	447519	U46258	Hs.339665	ESTs	4.4
	425916	NM_006786	Hs.162220	urokinase 2	4.3
	409420	Z15008	Hs.54451	laminin, gamma 2 (nolein (100kD), kalinin (10	4.3
25	416320	H47867	Hs.34024	ESTs	4.3
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth facto	4.3
	441582	BE650200	Hs.127197	ESTs	4.3
	414132	A801235	Hs.48480	ESTs	4.3
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to	4.3
30	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	4.3
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.3
	428613	AB037749	Hs.186928	KIAA1328 protein	4.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter tra	4.3
	447078	AW885727	Hs.301570	ESTs	4.3
35	434699	AA643897	Hs.149425	Homo sapiens cDNA FLJ11980 fs, clone HEMBB10	4.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.3
	405708		Target Exon	4.3	
	433405	AW157566	Hs.156892	ESTs	4.3
	456443	AW987500	Hs.133543	ESTs	4.3
40	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	4.2
	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU_HUMAN ALU SUBFAM	4.2
	412608	AA247996	Hs.44698	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
	406587	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.2
	455365	AW984343	Hs.194097	gb:RCO-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
45	452930	AW195295	Hs.194097	ESTs, Weakly similar to I38022 hypothetical p	4.2
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical p	4.2
	429305	AW449579	Hs.156739	Leptons XG mRNA (clone PEP11)	4.2
	427666	AI791495	Hs.180142	calfmodulin-like skin protein	4.2
	444602	AI174456	Hs.271925	ESTs, Moderately similar to I38022 hypothetical	4.2
50	417791	AW9565339	Hs.111471	ESTs	4.2
	444266	AI24984	Hs.125465	ESTs	4.2
	439394	AA149250	Hs.56105	ESTs	4.2
	457336	AW959657	Hs.281029	ESTs, Weakly similar to I38022 hypothetical p	4.2
	429125	AA446884	Hs.271004	NN_021048:Homo sapiens melanoma antigen, fami	4.2
55	404440		protein related with psoriasis	4.2	
	449228	AJ403107	Hs.148590	ESTs	4.2
	437144	AL049468	Hs.7859	ESTs	4.2
	448599	AW860912		gb:QVD-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like protein	4.2
60	419981	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.2
	444361	W78027	Hs.23820	hypothetical protein FLJ11105	4.2
	458116	AW977549	Hs.47367	KIAA1785 protein	4.1
	444105	AW189097	Hs.166587	ESTs	4.1
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	4.1
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor, cl	4.1
65	408086	BE250162	Hs.83765	dihydrofolate reductase	4.1
	457620	AA602711	Hs.336753	EST	4.1
	402048		Target Exon	4.1	
	427026	AA397589	Hs.97623	ESTs	4.1
70	423515	AA327017	Hs.162204	ESTs	4.1
	423891	AK020242	Hs.134795	Homo sapiens cDNA FLJ11180 fs, clone PLACE10	4.1
	455310	AW893961		gb:RC4-NN027-060400-011-d11 NN027 Homo sapi	4.1
	416636	AW959433	Hs.326290	hypothetical protein FLJ12581	4.1
	428642	AW058223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.1
75	423738	AB002134	Hs.132195	airway trypsin-like protease	4.1
	448243	AW389771	Hs.52820	integrin, beta B	4.1
	411559	BE144081		gb:MR0-HT0166-030200-007-d06 HT0166 Homo sapi	4.1
	423553	AA405635	Hs.95854	ESTs, Weakly similar to DYLYX_HUMAN CYTOPLASM	4.1
	457030	AJ301740	Hs.173381	dihydropyrimidinase-like 2	4.1
80	424415	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothetical p	4.1
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fs, clone PLACE10	4.1
	424745	AA214618	Hs.152759	activator of S phase kinase	4.0
	433384	AI021992	Hs.124244	ESTs	4.0
	448995	AI613276	Hs.5662	guanine nucleotide binding protein (G protein	4.0

	448504	AI858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
	424794	M85646	Hs.210695	ESTs	4.0
5	432184	AW971125	gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0	
	408321	AW405882	Hs.44205	cortistatin	4.0
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245571	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13987 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
15	416857	AA858115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	AI422017	gb:45f12.x1 NCL_CGAP_Bm23 Homo sapiens cDN	4.0	
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283381	ESTs	3.9
	454241	BE144666	gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9	
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177077	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959	AA122393	Hs.70811	NM_026001:Homo sapiens hypothetical protein	3.9
	428536	AI143139	Hs.22681	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi]	3.9
	432757	AF113013	Hs.276919	PRO0806 protein	3.9
30	418866	Z36830	Hs.87258	annexin A8	3.9
	437845	AA769578	Hs.90488	ESTs	3.9
	413801	MG2246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.8
	419312	AA831850	Hs.58149	hypothetical protein MGC14136	3.8
	429441	AJ224172	Hs.204096	lipophilic B (uteroglobin family member), pro	3.8
35	410563	AW016924	Hs.255527	hypothetical protein MGC14128	3.8
	444665	BE013126	Hs.47783	B aggressive lymphoma gene	3.8
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11871 fis, clone HEMBB10	3.8
	442163	AT791749	Hs.128896	ESTs	3.8
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.8
40	406560	AF005082	ENSP0000016943:CDNA	3.8	
	407395	AF005082	gb:Homo sapiens skin-specific protein (xp33)	3.8	
	404132		Target Exon	3.8	
	409601	AF237621	Hs.80828	keratin 1 (epidermolysis hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
45	433269	AF005258	gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8	
	436149	AT754308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bind)	3.8
	405545		(MDR/TAP) (TAP2)	3.8	
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409887	T81125	Hs.8493	ESTs	3.8
	407291	AA001464	gb:ze45b01.r1 Scores refine N2b4HR Homo sapie	3.8	
	415532	R14780	Hs.12026	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388	gb:3HSC1AF121 normalized infant brain cDNA Hom	3.8	
	438777	AA625487	Hs.142179	ESTs	3.8
	422938	NM_001609	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidemolysins bu	3.7
	405943		Target Exon	3.7	
60	430586	NM_001942	Hs.2633	desmoglein 1	3.7
	456242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418682	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465984	Hs.280720	ESTs	3.7
	449592	AI655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	RG4719	gb:EST22d11 WATM1 Homo sapiens cDNA clone '22d	3.7	
70	418735	NA8789	Hs.44609	ESTs	3.7
	444707	AI188013	Hs.41680	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055	gb:ln20g10.x1 NCL_CGAP_Ut1 Homo sapiens cDNA	3.7	
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
75	432837	AA310593	Hs.87329	HSPC072 protein	3.7
	442353	BE379534	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 ninein - mouse	3.7
	410784	AW003201	gb:JL2-UM0077-070500-080-E08 UM0077 Homo sapi	3.7	
80	409582	R27430	Hs.271585	ESTs	3.6
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kO)	3.6
5	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	CE36 gene	3.6
	413278	BE583085	Hs.833	Interferon-stimulated protein, 15 kDa	3.6
	420373	AW668228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
10	441436	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI031874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
15	434321	AA629368		gb:zu78a11.s1 Scores_tests_NHT Homo sapiens	3.6
	426514	BE616833	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 78	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullos pemphigoid antigen 1 (230/240kD)	3.6
20	426749	AI623718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin 1	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi]	3.6
	424927	AW873886	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin t	3.5
25	408867	AA437199	Hs.656	cell division cycle 25C	3.5
	428506	BE252363	Hs.184688	SBB131 protein	3.5
	431120	AA492588		gb:ng95c08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557:Homo sapiens keratin 16 (focal non	3.5
	408965	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
30	458671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 [HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.119991	ESTs	3.5
	431917	D16161	Hs.2868	peripheral myelin protein 2	3.5
35	443113	AI040586	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8688	ESTs	3.5
	407758	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Prl1 Homo sapiens cDNA	3.5
	423841	AW753867		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
40	408633	AW963372	Hs.46577	PRO2000 protein	3.5
	427878	C05788	Hs.181022	CG-07 protein	3.5
	419945	AW280975	Hs.118923	ESTs	3.5
	448372	AW445156	Hs.170802	ESTs	3.5
	407137	T97307		gb:yte53h05.s1 Scores fetal liver spleen 1NFLS	3.5
45	411274	NM_002770	Hs.69423	kalikrein 10	3.5
	400666			NM_002425:Homo sapiens matrix metalloprotein	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target_Exon	3.4
	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
50	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456298	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGCG3295	3.4
	429274	A179772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
55	419807	R77402		gb:yf75f11.s1 Scores placenta Nb2HP Homo sapi	3.4
	451778	A1828131	Hs.71243	ESTs, Weakly similar to zinc finger protein [3.4
	430397	A1824533	Hs.103607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23950	cyclin B1	3.4
60	455092	A152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	XG4942	Hs.83768	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648		nudin (nucleoside diphosphate linked moiety X	3.4
65	434208	AW136973	Hs.2B8516	ESTs, Weakly similar to S6B869 mitogen induc	3.4
	413219	A1878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.188287	much 4, tracheobronchial	3.4
	438893	AA828995		gb:cd77b08.s1 NCL_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target_Exon	3.4
70	435360	AF105386	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	428572	AB057763	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AK054680	Hs.171176	ESTs	3.3
	444910	A1201849		gb:yq76g04.x1 NCL_CGAP_Pr28 Homo sapiens cDNA	3.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp586A1046 (from c	3.3
75	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89548	selectin E (endothelial adhesion molecule 1)	3.3
	427660	A1741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE068	3.3
	419751	AW195581	Hs.93121	KIAAU0761 protein	3.3
80	404782			C7001892+gl6724096[gb]AAF26844.1 (AF195021	3.3
	415613	R20233		gb:yg18h11.r1 Scores infant brain 1NIB Homo s	3.3
	452198	AI097660	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406539			Target_Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

	412879	BE092219	gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55606 ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895 ESTs	3.3
	443903	AI220547	Hs.135228 ESTs	3.3
5	432015	AL157504	Homo sapiens mRNA; cDNA DKFZp586O0724 [from c	3.3
	447153	AA805202	Hs.315562 ESTs	3.3
	450769	AA057418	Hs.33654 ESTs	3.3
	421379	Y15221	Hs.103982 small inducible cytokine subfamily B (Cys-X-C	3.3
	402481		NM_001821*:Homo sapiens chromoderreria-like (R	3.3
	459394	BE408894	Hs.126522 Homo sapiens, clone MGC:16722, mRNA, complete	3.3
	424384	AW383226	Hs.201189 ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495 ESTs	3.3
	414869	AA157291	Hs.21479 ubiqulein 1 ESTs	3.3
15	441690	RB1733	Hs.33106 plaminogen activator, urokinase	3.3
	414774	X02419	Hs.77274 zinc finger protein	3.3
	412246	AI160873	Hs.69233 BE007967 ESTs	3.3
	412903	BE007967	Hs.155795 cadherin 3, type 1, P-cadherin (placenta)	3.3
	431958	X63629	Hs.2877 ESTs	3.3
	451177	AI989716	Hs.13034 gbt:zm86b09.r1 Stratagene colon HT29 (937221)	3.3
20	408990	AA070337	Hs.201189 ESTs	3.3
	418462	BE001596	Hs.85266 integrin, beta 4	3.3
	424687	J05070	Hs.151738 matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196		C2000802*:gtf7512792 pirf T12482 hypothetical	3.3
25	459267	AJ003631	gb:AJ003631 Selected chromosome 21 cDNA library	3.3
	432917	NM_014125	Hs.279812 PRO0327 protein	3.3
	440251	BE280466	Hs.84045 hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307 ESTs	3.3
	420218	AW958037	Hs.286 ribosomal protein L4	3.2
30	429594	AK001128	Hs.210297 Homo sapiens cDNA FLJ10266 fts, clone HEMBB10	3.2
	447762	AI939461	Hs.161370 ESTs	3.2
	414147	BE091634	gb:L2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917 dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323346 KIAA1008 protein	3.2
	402800		Target Exon	3.2
35	411263	BE297802	Hs.69380 kinesin-like 6 (mitotic centromere-associated	3.2
	424308	AW975531	Hs.154443 minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450	gb:PM4-SN0020-0-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362	gb:30g7 Human retina cDNA randomly primed sub	3.2
	401458		Target Exon	3.2
40	432361	AI378562	Hs.159585 ESTs	3.2
	444008	BE544865	Hs.220756 ESTs, Weakly similar to SFR4_HUMAN SPlicing F	3.2
	405336		Target Exon	3.2
	446563	BE32658B	Hs.141454 ESTs	3.2
45	449278	AW241510	Hs.252713 ESTs	3.2
	455838	BE145808	gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
	420591	X53655	Hs.99171 neurotrophin 3	3.2
	401486		C4000647*:gb 4758508 ref NP_004253.1 airway	3.2
	432979	AA573263	Hs.120860 ESTs	3.2
50	413633	Z16005	Hs.75573 centromere protein E (312kD)	3.2
	438325	AA804258	Hs.123229 ESTs	3.2
	421751	AW813731	Hs.159153 ESTs, Moderately similar to S6567 alpha-1C-a	3.2
	431938	AA938471	specific granule protein (28 kDa); cysteine-rich	3.2
	421777	BE562088	HSPC037 protein	3.2
	408113	T82427	Hs.194101 Homo sapiens cDNA: FLJ20869 fts, clone ADKA02	3.2
55	427359	AW020792	Hs.79881 Homo sapiens cDNA: FLJ23008 fts, clone LNGD04	3.2
	402337		Target Exon	3.2
	420830	AW886650	gb:CM4-NT0007-130500-551-006 NT0007 Homo sapi	3.2
	438168	AK000883	Hs.301645 Homo sapiens cDNA FLJ10021 fts, clone HEMBA10	3.2
	443428	AF098158	chromosome 20 open reading frame 1 ESTs	3.1
60	437641	AA811482	Hs.201911 enhancer of zeste (Drosophila) homolog 2	3.1
	414761	AU077228	Hs.77258 hypothetical protein PRO2176	3.1
	434208	T92641	Hs.127648 ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
	432222	AW514472	Hs.238415 hypothetical protein MGC16207	3.1
65	452934	AA581322	Hs.4213 regulatory factor X-associated protein	3.1
	458923	Y12812	Hs.24422 gamma-aminobutyric acid (GABA) A receptor, epsilon	3.1
	448988	Y09763	Hs.22785 Homo sapiens mRNA full length insert cDNA clone	3.1
	439750	AI359053	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
	422283	AW411307	Hs.114311 KIAA1803 protein	3.1
	445885	AI734009	Hs.127689 Homo sapiens cDNA: FLJ21814 fts, clone HEP010	3.1
70	441962	AW972642	calcium/calmodulin-dependent serine protein k	3.1
	424653	AW977534	gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	431322	AW070622	forkhead box E1 (thyroid transcription factor	3.1
	423934	U69995	gb:RC3-HT0800-240400-023-g05 HT0800 Homo sapi	3.1
	455987	BE178323	Home sapiens, clone IMAGE:3939163, mRNA, part	3.1
75	421426	AA291101	Hs.33020 DKFZP434G232 protein	3.1
	423887	AL080207	Hs.134585 ESTs	3.1
	408295	AI117452	Hs.44155 DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084 ESTs	3.1
	441974	AI683782	Hs.128245 ESTs	3.1
80	446474	AI301227	Hs.150186 hypothetical protein DKFZp586K1946	3.1
	452166	AB948607	Hs.204680 ESTs	3.1
	451659	BE379761	Hs.14248 ESTs	3.1
	439979	AW600291	Hs.6823 hypothetical protein FLJ10430	3.1

5	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
	449441	AI656040	Hs.196532	ESTs	3.1
	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167589	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
10	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT2RP30	3.1
	422168	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	H46739		gb:y14h02.s1 Soares adult brain N2b5HB35Y Ho	3.1
	426081	X74794	Hs.154443	minichromosome maintenance deficient (S. cerev)	3.1
	404107			Target Exon	3.1
15	419563	AA528235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L121 (from c	3.1
	435604	AA625279	Hs.28692	uncharacterized bone marrow protein BM040	3.1
	442824	BE178056	Hs.144031	ESTs	3.1
	435081	AI651474	Hs.163944	ESTs	3.1
20	420589	AA419360	Hs.192708	ESTs	3.0
	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
	406087			Target Exon	3.0
25	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163800	ESTs	3.0
30	446733	NM_005829	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wg05002x1 NCL_CGAP_Kgd12 Homo sapiens cDN	3.0
	413281	AA661271	Hs.222024	transcription factor BWA12	3.0
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2B10027O1	3.0
	445505	AJ971156	Hs.148891	ESTs	3.0
	426005	AI568551		gb:tn07g03.x1 NCL_CGAP_Bm25 Homo sapiens cDN	3.0
	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
40	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AI040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE076114	Hs.300722	gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
	417734	Z42657	Hs.6724	ESTs	3.0
45	449576	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511		ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:UH-B-H2-eh2-h-03-0-ULs1 NCL_CGAP_Sub4 Ho	3.0
	444477	AI150548	Hs.23155	ESTs	3.0
50	448255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gi 7513113 pir T13078 KIAA0892 pro	3.0
	450841	AI741468	Hs.270515	ESTs	3.0
	410581	BE540265	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
	433871	W02410	Hs.205555	ESTs	3.0
55	401994			Target Exon	3.0
	449272	AW137656	Hs.197845	ESTs	3.0
	409703	NM_008187	Hs.56008	2'-S-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
60	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	GE284633	Hs.143638	WD repeat domain 4	3.0
	432220	AI571306	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:hb75d03.x1 NCL_CGAP_U12 Homo sapiens cDNA	3.0
65	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG repeat	3.0
	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; br	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukaemia factor 1	3.0
70	433485	AI493078	Hs.201957	aldo-keto reductase family 1, member C2 (dky	3.0
	423556	R72894	Hs.7720	dynamin, cytoplasmic, heavy polypeptide 1	3.0
	426880	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.138672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20610	2.9
	402556			C1001383:gi 538695 pir A61183 hypothetical	2.9
75	411098	AW817238		gb:Q00-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	436399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427985	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
	410658	AW105231	Hs.192035	ESTs	2.9
80	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TC8AP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621* Keratin, type II cytoskele	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

	456318	AW895387	gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ04672	Hs.334483 hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118664 ESTs	2.9
	432215	AU076609	Hs.2934 ribonucleotide reductase M1 polypeptide	2.9
5	434423	NM_008769	Hs.3844 LIM domain only 4	2.9
	446269	AW263155	Hs.14559 hypothetical protein FLJ10540	2.9
	412367	AW945964	Hs.2934 gb:QVO-ET0001-050500-220-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583 Homo sapiens cDNA FLJ20779 fs, clone COLD507	2.9
10	421190	U95031	Hs.102482 mucin 5, subtype B, tracheobronchial	2.9
	404981	AA147829	Hs.301431 ENSP0000252242*:Keratin, type II cytoskeletal	2.9
	448796	AA147829	Hs.301431 endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449 Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760		Target Exon	2.9
	443859	NM_013409	Hs.9914 follistatin	2.9
15	404253		NM_021058*:Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635 hypothetical protein DKFZp434K2435	2.9
	435887	AA954229	Hs.114052 ESTs	2.9
	429036	BE549781	Hs.270475 ESTs	2.9
20	446733	AA863360	Hs.26040 ESTs, Weakly similar to fatty acid omega-hydri	2.9
	446417	AI299050	gb:gn14d12.x1 NCL_OGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ003029	Hs.65792 synaptophysin, gamma 2	2.9
	452452	BE393822	Hs.29645 Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178 hypothetical protein FLJ23488	2.9
25	450698	W31489	Hs.95044 ESTs, Weakly similar to I38022 hypothetical p	2.9
	439430	AF124250	Hs.6564 cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460 Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502 ESTs	2.9
	401781		Target Exon	2.9
	439825	AF086453	Hs.58611 ESTs	2.9
30	425234	AW152225	Hs.165909 ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153 ESTs	2.9
	414915	NM_002462	Hs.76391 myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AI668594	Hs.176588 ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
35	443479	AF027219	Hs.9443 zinc finger protein 202	2.9
	442601	AI684969	Hs.46772 ESTs	2.9
	405932		C16000305:gi 3806122 gb AAC89198.1 (AF097887	2.9
	405454		C12000541:gi 5729984 ref NP_00539.1 IGF-II	2.9
	418844	M62982	Hs.1200 arachidonate 12-lipoxygenase	2.9
40	408562	AI436323	Hs.31141 Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.48384 heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010 ESTs	2.9
	411268	AK000512	Hs.69388 hypothetical protein FLJ20505	2.9
	450024	AA005129	gb:zh90h08r1_Soares_fetal_liver_spleen_1NFLS	2.9
45	400297	AI127076	Hs.334473 hypothetical protein DKFZp564C1278	2.9
	436481	AA379597	Hs.5199 HSPC150 protein similar to ubiquitin-conjuget	2.9
	400631	AF173937	Hs.109494 secreted protein of unknown function	2.9
	429118	H20669	Hs.35406 ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713 ESTs, Weakly similar to S64054 hypothetical p	2.9
	435711	AF226667	Hs.58553 CTP synthase II	2.9
50	419088	AI538323	Hs.52820 Integrin, beta 8	2.8
	431629	AU077025	Hs.265827 interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984 hypothetical protein MGC13102	2.8
	451702	AW685452	Hs.246503 ESTs	2.8
55	432162	AA584052	Hs.272798 hypothetical protein FLJ20413	2.8
	405281	BE080028	Hs.20158 NM_022864:Homo sapiens pregnancy-zone protein	2.8
	438161		ESTs, Weakly similar to S34169 transcription	2.8
	409103	AF251237	Hs.112208 XAGE-1 protein	2.8
	425599	AW36745	Hs.214140 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
60	426274	BE281191	Hs.155462 minichromosome maintenance deficient (miss, S	2.8
	435099	AC004770	Hs.4756 flap structure-specific endonuclease 1	2.8
	445873	AA250970	Hs.251946 poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216 ESTs	2.8
	413083	BE064528	gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
65	437030	AA742577	Hs.303781 E8T	2.8
	438113	AI467908	Hs.8882 ESTs	2.8
	442973	BE567685	Hs.288550 Homo sapiens cDNA: FLJ23158 fs, clone LNG096	2.8
	440994	AI160011	Hs.193341 ESTs	2.8
	442295	AI827248	Hs.224398 Homo sapiens cDNA FLJ11469 fs, clone HEMBA10	2.8
70	422689	AW856665	Hs.285665 gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192 coagulation factor III (thromboplastin, tissu	2.8
	424408	AI754813	Hs.146428 collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.161275 ESTs	2.8
	403806		Target Exon	2.8
	437182	AI080098	gb:Homo sapiens mRNA; cDNA DKFZp564C1072 (fr	2.8
75	453955	AW579207	Hs.304666 ESTs, Weakly similar to 178885 serine/threon	2.8
	420795	AA323037	Hs.128645 sorting nexin 16	2.8
	452696	AI826645	Hs.211534 ESTs	2.8
	432656	NM_000246	Hs.3076 MHC class II transactivator	2.8
80	438052	AA776564	Hs.41891 zinc finger 1111	2.8
	441755	AW450926	Hs.127786 ESTs	2.8
	427981	AW293165	Hs.143134 ESTs	2.8
	449785	AI225235	Hs.288300 hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072 ESTs	2.8

	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 4DS RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.8
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
5	448979	A1611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410654	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250716	Hs.87614	ESTs	2.8
10	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	A1267371	Hs.172636	ESTs	2.8
	469719	AW749511	Hs.301564	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
15	428301	AW628866	Hs.98440	ESTs, Weakly similar to J38022 hypothetical p	2.8
	403000	BE247275	Hs.161787	U6 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	TG3959	Hs.228320	hypothetical protein FLJ23537	2.8
20	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
	456091	BE079752	gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8	
	410049	AW579475	gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8	
	452571	W31518	Hs.34685	ESTs	2.8
	455666	BE055813	gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8	
25	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarco(glycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50768	SMC4 [structural maintenance of chromosomes 4	2.7
	418992	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
30	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA1D	2.7
	433345	AI681545	Hs.162982	hypothetical protein FLJ13117	2.7
	403763			NM_001059:Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetical	2.7
	406753	AA505665	Hs.217493	annexin A2	2.7
35	415747	AA381208	gb:ESTB4257	Activated T-cells 1 Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW804176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430488	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
	456181	L36453	Hs.1030	ras inhibitor	2.7
40	416548	H62953		gb:cyt47705.1 Soares fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGER	2.7
	417398	N78541	Hs.177366	ESTs	2.7
45	408380	AF123060	Hs.44532	diubiquitin	2.7
	437724	AW444826	Hs.184923	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363	gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7	
	441352	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli RecA ho	2.7
50	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
	408092			Target Exon	2.7
	447748	AI220203	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
55	433743	AF075312	Hs.235760	Homo sapiens clone HQ0262	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	405675			Target Exon	2.7
	424825	AW004466	Hs.321197	PDZ domain protein (Drosophila InaD-like)	2.7
	416250	AA681386	Hs.73452	hypothetical protein MGC10791	2.7
	448892	N69546	Hs.44563	hypothetical protein	2.7
60	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
	407287	AI678812	Hs.203349	gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20630	kinase-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
65	417357	AF280257	Hs.131917	retinitis pigmentosa GTPase regulator Interac	2.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	DB6980	Hs.79170	KIAA0227 protein	2.7
	458201	AI999981	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
70	401230			NM_014191:Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234642	aqueaporin 3	2.7
	444006	BE098085	Hs.10086	type I transmembrane protein Fn14	2.7
75	443500	AV646386	Hs.93961	Homo sapiens mRNA; cDNA DKF2p667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AW986268	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
	418889	AW516565		gb:cx01d05.x1 Soares_NHCCeC_cervical_tumor Hom	2.7
	431688	AA513906		gb:ng57c08.s1 NCL_CGAP_Lip2 Homo sapiens cDNA	2.7
80	427579	AA366143	Hs.178689	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	A160386	Hs.125037	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AJ355361	Hs.228376	ESTs	2.6
	419833	AA251131	Hs.220697	ESTs	2.6
	411819	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi		2.6
	445592	AV654382	Hs.17947	ESTs, Weakly similar to I36534 hypothetical p	2.6
5	446102	AW168067	Hs.252950	ESTs	2.6
	441408	AJ73249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transe	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27498	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual arachnod	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276886	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
15	433288	AJ368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AJ753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW884542	gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi		2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [Hs	2.6
	401260	C1001031*;gi 7305041 ref NP_036876.1 erythro			2.6
20	435135	R27299	Hs.10172	ESTs	2.6
	412108	AA100283	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA988176	Hs.121553	hypothetical protein FLJ20541	2.6
	408594	AA076118	gb:cmr10e08.s1 Stratagene pancreas (937208) Ho		2.6
	410008	AA079552	gb:cmr20h12.s1 Stratagene pancreas (937208) Ho		2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
30	405671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AJ765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF148074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663	gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi		2.6
	408625	AW243323	Hs.286785	ESTs	2.6
35	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ecto	2.6
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	connexin protein F (350/400kD, milosin)	2.6
	401050			NM_014155*;Homo sapiens HSPC053 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE082900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z185_HUMAN ZINC FINGER	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903*;Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	425698	NM_018112	Hs.159241	polycystic kidney disease 2-like 1	2.6
50	424783	AA813909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425602	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452221	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U80304	Hs.25351	Iniquous homeobox protein 6	2.6
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
55	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0362 Homo sapi	2.6
	427089	AB032953	Hs.173500	odd Ozflier-m homolog 2 (<i>Drosophila, mouse</i>)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52954	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
	453331	A1240665	Hs.8895	ESTs	2.6
60	447175	AI365208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288988	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
65	434567	AW8555466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
	418067	AH127858	Hs.83393	cystatin E/M	2.6
70	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55644		gb:Human spleen PABL (pseudoautosomal bounder	2.6
75	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
	419663	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp583E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp43401214 (from c	2.6
	425415	M13903	Hs.157091	Involucrin	2.6
	444826	AI674482	Hs.148441	ESTs	2.6
80	413331	BE083950		gb:PM0-BT0551-260200-001-b11 BT0651 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706*;gi 1345852 sp P15989 CA38_CHICK COL	2.6
	413964	BE175582		gb:RC5-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979704		gbEST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.338951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1589	LIM homeobox protein 2	2.5
	411171	AW820260		gb:CV2-ST0296-190200-040-c10 ST0296 Homo sapi	2.5
	447197	R26075		gb:RyBbb01.s1 Soares placentia Nb2HP Homo sapi	2.5
	459688	U72571	Hs.151250	Intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE059288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AAB85108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW594222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
15	409676	AA077118	Hs.197298	NS1-binding protein	2.5
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201977	DESC1 protein	2.5
	424420	BE014743	Hs.146683	prostaglandin E synthase	2.5
	427610	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
20	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455096	AW855598		gb:CM1-CT0278-031199-032-e0B CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
25	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035261	Hs.61753	ESTs	2.5
30	438533	AI440286	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412319	AW336832		gb:PM2-DT0023-050403-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	AL119671	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
35	434913	AW72850	Hs.11056	RALBP1 protein	2.5
	448946	AI652655	Hs.23383	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
	448344	AI640355	Hs.312691	ESTs	2.5
	438436	BE140845	Hs.57686	ESTs	2.5
	449867	A672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
45	433675	AW977853	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766	Hs.1657	ESTs	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	ESTs	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	A761324		gb:W60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	A101456	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71879	Interleukin 19	2.5
55	436661	AW376974	Hs.155704	ESTs	2.5
	431124	AF284221	Hs.59508	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
60	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300592	v-myc avian myeloblastosis viral oncogene hom	2.5
	442886	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	A789444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA817808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:CV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI653240	Hs.49823	ESTs	2.5
	428780	AJ476578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.5467	synaptojanin 3	2.5
75	422555	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fascin h	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.86663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AI053464	Hs.166505	ESTs	2.5
80	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
	438214	H06076	Hs.26320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76034	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

	Pkey	CAT number	Accessions
10	407642	1007176_1	AW178993 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806959 AW845686 BE141054 BE141040 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968
15	408391	1055687_1	AW859276 AW859274 AW190959 T91463
	408650	107490_1	AW884542 AA056567 AW882724
	409594	114249_1	AA076118 AA976618 AA076220
	409895	114076_1	AA296961 AA296889 AA076945 AA077528 AA077497
	409990	116644_1	AA079337 AA079338 AW272100
20	410008	116812_1	AA079552 BE142625 BE142527
	410049	1172307_1	AW579476 AW939664 AW939655
	410784	1221005_1	AW803204 BE079700 BE062940
	411098	1232093_1	AW817238 AW993885 AW993998
	411171	1234393_1	AW820260 AW820332 R94406
25	411465	1246769_1	AW847683 AW847861 AW861080
	411559	1249417_1	BE144081 BE144190 AW851155
	411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	411858	126717_1	AA099020 AW751275 AW751276 AW751289
	412279	1287332_1	BE245511 BE246133 AW935247
30	412313	1288355_1	AW936682 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936683 AW935777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936659 AW936536 AW936774 AW936778 AW936766
	412333	1289037_1	AW937465 AW937569 AW937658 AW937654 AW937492
35	412367	1291505_1	AW945938 AW946020 AW946034 AW948027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW948036
	412879	1334272_1	BE092219 BE092381 BE066789
	413083	1346639_1	BE064529 BE064589 BE064561
	413331	1361726_1	BE083950 BE084017 BE084016
	413864	1395788_1	BE175592 BE175514 BE175505 BE175591 BE175530
40	414147	142127_1	BE091634
	414148	142133_1	BE084049 AW292907 AA135984
	416317	1533847_1	Z43388 F05453 R19573 R20275 H06917
	416813	1540602_1	R20233 F12901 T74740
45	415747	155189_1	AA381209 AA381245 AA167683
	416120	157126_1	H46739 H51513 H19779
	416168	1574545_1	H23687 H46480 H40239
	416848	1600161_1	H29533 N76608 N72413
	417742	1696282_1	R64719 Z44680 R12451
	418347	174149_1	AA216419 F03238 AA229517
50	418869	179863_1	AW516565 AA229762 AA230035
	419807	188252_1	R77402 AA262462 AA260988 R06794
	420373	193194_1	AW968228 AA259146 W01465
	420637	195241_1	AW876163 AA278946 AA747691
55	420830	197736_1	AW888850 AW880651 BE149946 BE149948 BE149951 BE149947 AW888849 AA281840 AA281822 AW888852
	422699	219398_1	AW856665 AA315008 AW954733
	423733	231476_1	AA330281 AA330232 AW952521
	423735	231498_1	AA330263 AA651805 AA502431 AW974633 AA649496
	423841	232507_1	AW753967 AA370795 AA331630 AW962550
60	425005	245908_1	AI565851 AA348656 R24798
	425163	300543_1	AA884766 AW974271 AA592975 AA447312
	431120	328264_1	AA492588 AA492498 AA492571
	431322	331643_1	AW970822 AA503009 AA502998 AA502889 AA502805 T92188
	431698	336609_1	AA513906 AA847734 AA357044
	432184	342677_1	AW971125 AA527731 N52655 AI621608 AA532420
	432189	342819_1	AA527941 AI620608 AI620190 AA635266
	432869	355475_1	AW974094 AA569074 AA602574
	433289	36202_1	AF006258
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 B6348834 AW170383 AA600968 AA778832
	433644	371919_1	AW342028 AA641080 AA603282
70	434321	383473_1	AA629368 AW848574 AW984953
	435399	405576_1	AA679463 AW813779 AW813709
	437182	43421_1	AL080098 AL037472 AA432051
	437938	44573_2	AI950067 N70208 R97040 N38809 AI308119 AW967577 N35320 AI251473 H59397 AW971573 R97278 W01059 AW957671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71458 T82391 BE328571 T75102 R34726 AA884922 BE328617 AI219788 AA884444 N92578 F13493 AA927794 AI565025 AW874068 AL134043 AW235633 AA683345 AW008222 AA488954 AA283144 AI90397 AI950344 AI741346 AI689062 AA282915 AW102888 AI872193 AI763273 AW173586 AW160329 AI653832 AI762688 AA988777 AA488982 AI356394 AW103813 AI539842 AA642789 AA856975 AW505512 AI981530 AW629970 BE612681 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337493 AW961101 AA251683 AA251874 AI619225 AW05882 AI683338 AI658509 AW276905 AI633006 AA972584 AA908741 AW72629 AW513996 AA293273 AA969759 N75828 N22388 H84725 H60052 T92487 AI620256 AA780419 AA551005 W07071 AW613456 AI373032 AI564269 F00831 H83468 W37181 W78802 R66056 AI002839 R57640 AA300207 AW959581 T63226 F04005
75	438390	45662_1	AI422021 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AM423279 AI423645 AI424090 AI359637 AL044792 D17003
	438666	467436_1	AI979074 AA894841 AA828650
	438993	467651_1	AA828995 AA834987 AI926381

	439579	47404_1	AF086400 W79232 W73990
	440320	491930_1	AA879294 NG7538 A1474541
	444910	624951_3	A1201849 BE069007 AW946544
	446417	676384_1	A1290950 BE256910
5	447197	711623_1	R36075 A1366546 R36167
	448699	770766_1	AW860912 A1540666
	449034	794817_1	AH624049 AW117770 A1858360
	450024	82298_1	AA005129 AA679084 AA694399
10	450613	840016_1	A1702055 R89208 R86260
	451105	859083_1	A7761324 AW80941 AW809037
	451153	86054_1	BE092900 AAU15577 AA018521
	451340	86640_1	AW936273 AW340350 AA017208
	454202	1050507_1	AW178363 AW846011 AW845964 AW845988 AW845977 AW846002
15	454241	1067807_1	BE144666 BE184942 AW238414 BE184946
	454707	1230250_1	AW814989 AW814852 AW814808
	454891	1239217_1	AW837349 AW837355 AW882717
	454988	1248607_1	AW850140 AW850195 AW850192
	455091	1252939_1	BE079752 BE079868 BE148989 AW855332 BE148818 BE148815 BE148796
20	455092	1252971_1	BE152428 AWB55572 AW855607
	455095	1252987_1	AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605
	455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455319	1279172_1	AW895387 AW895647 AW895564 AW895323 AW895405 AW895539 AW895538
25	455385	1284681_1	AW94B343 AW94B341 AW902855 AW894737
	455549	1324695_1	AW994222 AW994377
	455666	1349545_1	BE065813 BE065788 BE065689 BE065832
	456750	1355998_1	BE075114 BE075283 BE075116
	455839	1374605_1	BE145808 BE145807 BE181883
30	455987	1397735_1	BE178323 BE177978
	457405	333127_1	AA504860 AA504911
	458829	773443_1	AI557386 BE158936
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 12C

35	Pkey:	Unique number corresponding to an Eos probeset.		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-496.		
	Strand:	Indicates DNA strand from which exons were predicted.		
40	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
45	400612	9929646	Minus	151513-151662
	400666	8118496	Plus	17982-18115,20297-20456
	401050	8117628	Minus	78449-79425
	401137	2547238	Minus	598-1009
	401230	9929527	Minus	33836-34006,34538-34592,38461-36745,48925-49095,52604-52758
	401260	8076883	Minus	88008-88355
50	401357	9788198	Minus	145356-145807
	401458	9187886	Plus	76485-77597
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
	401575	7229804	Minus	76263-76384
	401747	8789672	Minus	118598-118816,119119-119244,119609-119781,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132875,133580-134011
55	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28517,288920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-B3435,83531-83656,B3740-B3901,84237-84393,84955-85037,86290-86814
	401894	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
60	402048	8072512	Plus	43936-44078
	402298	6598824	Plus	35758-37953
	402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
	402481	9797406	Plus	87681-88991
	402556	9863723	Plus	13579-14026
65	402638	9958129	Minus	20167-22383
	402800	6010175	Plus	43921-44049,46181-46273
	402892	8088844	Minus	194384-194645
	403274	8072441	Minus	104059-104179,105563-106859
	403471	9930659	Minus	85867-85983
70	403763	7229888	Minus	43575-43867
	403808	8140491	Plus	146390-146878
	403983	8576058	Minus	82441-82701
	404107	8099028	Minus	201699-202363
	404132	6981900	Plus	11307-12434
75	404184	4581418	Minus	12652-13548
	404253	9367202	Minus	55675-56055
	404440	7528051	Plus	80430-81581
	404782	9910094	Minus	15455-15589
	404959	7407984	Plus	45243-45368
80	404981	4432779	Minus	20826-20770,22813-22721
	404986	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405041	7547195	Plus	121230-121714
	405196	7230083	Minus	135716-136851

	405277	3980473	Plus	23471-23572
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-46958,47298-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405336	6094635	Plus	33267-33563
	405454	7656675	Plus	133807-134063
5	405545	1054740	Plus	118577-118907,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	405657	4827303	Minus	104132-104293
	405675	4557087	Plus	70304-70630
10	405708	4166182	Plus	55030-55604
	405897	6758795	Plus	59828-60535
	405932	7767812	Minus	123525-123713
	405943	6758796	Plus	20605-20812
	406087	9123919	Minus	7234-7628
15	406092	9123919	Plus	251370-251797,252168-252982
	406467	8795551	Plus	182212-182958
	406554	7711566	Plus	106956-107121
	406560	7711569	Minus	35162-35292
	406599	8248616	Plus	10933-11086

20

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

25

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. Ig, fn3, egt, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

30

Pkey: Unique Ecs probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	PPDomains	Unigene Title	R1
40	425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_terminus	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83189	SS,hemopexin,Pepidase_M10	matrix metalloproteinase 1 (matrix metalloproteinase inhibitor 13) [interstitial]	38.9
	439606	W79123	Hs.58661	TM,7tm_1	G protein-coupled receptor 87	28.8
	452240	A159147	Hs.61232	TM	ESTs	27.0
45	424046	AF027855	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
	400289	X07820	Hs.2258	hemopexin,Pepidase_M10	matrix metalloproteinase 10 (stromelysin)	20.5
	418345	AJ01838	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13 (P113; se)	20.1
	423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
	428227	AA321649	Hs.2248	SS,TM,ILB	small inducible cytokine subfamily B (Cys)	15.9
	447164	AF026941	Hs.17518	TM,ILB	Homo sapiens cig5 mRNA, partial sequence	13.8
50	414764	AW013887	Hs.72047	TM	ESTs	12.9
	418661	AA634543	Hs.79440	TM	ICF-II mRNA-binding protein 3	12.7
	427585	D31152	Hs.179729	SS,C1q,Collagen	collagen type X, alpha 1 (Schmid metaphe)	12.6
	406467			TM,efhand	Target Ecn	10.5
55	428368	BE440042	Hs.83326	SS,Pepidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1)	10.2
	418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	-9.4
	419247	S65791	Hs.89764	TM,KH-domain	fragile X mental retardation 1	9.1
	446232	A1281848	Hs.194891	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-related ki	8.9
	422420	UD3358	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamily	8.7
60	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
	443432	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
	422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
	447342	A198268	Hs.19322	SS,lpocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
65	407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_terminus	ESTs	6.6
	410153	BE311926	Hs.15830	SS,Pepidase_M10,hemopexin	hypothetical protein FLJ12691	6.5
	414812	X72755	Hs.77367	SS,TM,ILB	monokine induced by gamma interferon	6.4
	421773	W692233	Hs.112457	SS	ESTs	6.2
	413395	M34455	Hs.840	TM,IDO	Indoleamine-pyrmale 2,3 dioxygenase	5.9
70	413763	U17760	Hs.75517	SS,Jammin_EGF,Jammin_Nterm,adh_short	laminin, beta 3 (lncn (125kD), kelin	5.8
	432239	XB1334	Hs.2936	SS,Pepidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
	418653	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
	407366	AF026942		TM,ILB	gb:Homo sapiens cig33 mRNA, partial seque	5.5
	433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
75	408536	AW381532	Hs.135188	SS,TM,E2-E2_ATPase,Calponin_ATPase_C, N	ESTs	5.4
	420440	NM_002407	Hs.97644	SRCRU,froglobin	memmaglobin 2	5.2
	437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
	405547			SS,TM,ABC_membrane,ABC_tran,Ig	NM_018633+Homo sapiens transporter 2, AT	5.1
	439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
80	426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
	423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
	426350	NM_003245	Hs.2022	TM,transglutaminase_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protel	5.0
	409744	AW675258	Hs.55265	TM,metallo,Keilich	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

	444461	RS3734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
	410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon- λ	4.8
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
	450375	AA009647	Hs.8860	TM,disintegrin,Pop_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domai	4.8
5	401575	NA		TM	Target Exon	4.6
	428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
	431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
	434899	AA643687	Hs.149425	TM,Nucleoside_trx2	Homo sapiens cDNA FLJ11980 (s, clone HEM	4.3
10	406667	M31125	Hs.272520	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
	404440			TM,MAGE	NM_021048;Homo sapiens melanoma antigen,	4.2
	449228	AJ403107	Hs.146690	TM,PAF-AH,p450	protein related with psoriasis	4.2
	444105	AW189097	Hs.166597	TM,cadherin	ESTs	4.1
	409632	WT4001	Hs.65279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
15	423515	A3227017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
	423553	AA106535	Hs.96854	TM	ESTs, Weakly similar to DYLX_HUMAN CYTOPL	4.1
	445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
	446689	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
20	428536	A1143139	Hs.2288	TM,efhand,Syndecan	visfatin-like 1	3.9
	413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
	429441	AJ224172	Hs.204098	Uteroglobin	lipophilin B (uteroglobin family member),	3.9
	409601	AF237621	Hs.80828	TM,filament,filament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	TM	ESTs	3.8
25	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	405645			SS,TM,proteasome,lg,ABC_memb,tranABC_tran,	(MDR/TAP) (TAP2)	3.8
	422936	NM_001809	Hs.1594	TM,thiokase	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	SS,TM,f3,vwa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolysl	3.7
30	430686	NM_001942	Hs.2633	SS,TM,cadherin,Cadherin_C_term	desmoglein 1	3.7
	444707	AJ188613	Hs.41690	TM,cadherin	desmocollin 3	3.7
	409582	R27430	Hs.271565	TM	ESTs	3.6
	408771	AW732573	Hs.47584	TM,K_tetra,Ion_trans	potassium voltage-gated channel, delayed-	3.6
	400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
35	413278	BE583085	Hs.833	TM,ubiquitinamin_G-leminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
	426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
	424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	SS,TM,Uteroglobin	mammaglobin 1	3.5
	407756	AA116021	Hs.36260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
	407137	T97307		TM,GDA1_CD39	gbeye53h05s.1 Soares fetal liver spleen 1	3.5
40	411274	NM_002776	Hs.69423	Igtpsin	kallikrein 10	3.5
	400686			SS,hemopexin,Peptidase_M10	NM_002425;Homo sapiens mabix,matrix metalloprot	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_Itransf_3,Cam_acyltransf	endothelial cell growth factor 1 (platele	3.4
	450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
45	451778	AI026131	Hs.71243	Ig	ESTs, Weakly similar to zinc finger pro	3.4
	430397	AI024533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
	449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
	422487	AJ010901	Hs.198267	TM,wwd	mucin 4, tracheobronchial	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
50	418984	AA266520	Hs.85646	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
	421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
	41774	X02419	Hs.77274	SS,kingle,trypsin	plasminogen activator, urokinase	3.3
	431958	X63628	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin, 3, type 1, P-cadherin (placental	3.3
	418462	BE001596	Hs.85266	SS,TM,integrin_B,fm3	integrin, beta 4	3.3
	424887	J05070	Hs.151738	SS,Peptidase_M10,fm2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
55	401486	NA		SS,TM,trypsin	C4000647;gi4768509;ref NP_004253.1 air	3.2
	408113	TS2427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 (s, clone AD	3.2
	427359	AW020782	Hs.79881	TM,7tm_3	Homo sapiens cDNA: FLJ23008 (s, clone LN	3.2
	452934	AA581322	Hs.4213	SS,TM,ig	hypothetical protein MGC16207	3.1
60	446988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
	439750	AL359053	Hs.57664	TM,integrin_B,Ricin_B_lectinnm	Homo sapiens mRNA full length insert cDNA	3.1
	414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
	435604	AA625279	Hs.26892	TM	uncharacterized bone marrow protein BM040	3.1
	453883	AI638516	Hs.22630	TM,Ets_SAM_PNT	cofactor required for Sp1 transcriptional	3.0
65	448733	NM_005629	Hs.187958	SS,TM,SNF_ABC_tran,Isoch,phkase,DSPc,Ribosomal_	solute carrier family 6 (neurotransmitter	3.0
	449448	AW139205	Hs.156457	SS,TM,abhydrolease	hypothetical protein FLJ22408	3.0
	437938	AI950087	Hs.57664	TM,histone,ig,MHC_I	gbwxq5c02.x1 NCI_CGAP_Ka12 Homo sapiens	3.0
	424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
	427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
	409703	NM_005187	Hs.56009	SS	2'-Oligoadenylate synthetase 3 (100 kD	3.0
70	447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P186 mRNA, CAG repe	3.0
	431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
	446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
	421190	M95031	Hs.102462	TM,ywd	myelin 5, subtype B, tracheobronchial	2.9
	452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
	443859	NM_013409	Hs.9914	SS,kazal	follistatin	2.9
	446733	AA8653360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
75	414581	AA256213	Hs.72010	TM,Cam_ecytransf,Choline_kinase,SCO1-6enC	ESTs	2.9
	431628	AU077025	Hs.265827	SS,IRNA_an6SH2,SH3,phkase	Interferon, alpha-inducible protein (cbo	2.8
	445873	AA260970	Hs.251946	SS,rrn,PABpkhase,14-3-3,rrn	poly(A)-binding protein, cytoplasmic 1-6	2.8
	438113	A1467908	Hs.8882	TM,7tm_1	ESTs	2.8
	410910	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

			SS,TM	gamma-aminobutyric acid (GABA) A receptor	2.8
			TM,g_pkase	sterol-koop (histone) binding protein	2.8
			TM,SCAN7tm_1	KIAA0036 gene product	2.8
			SS	hypothetical protein FLJ13117	2.7
5	452234	AI681645	Hs.152982	ESTs, Weedy similar to I38022 hypothetical	2.7
	452234	AW084176	Hs.223296	ras inhibitor	2.7
	456181	L38463	Hs.1030	diubiquitin	2.7
	408380	AF123050	Hs.44532	frizzled (Drosophila) homolog 6	2.7
	422278	AF072873	Hs.114218	mitotic spindle coiled-coil related prote	2.7
10	446839	BE091926	Hs.16244	hypothetical protein MGC10791	2.7
	416250	AA581386	Hs.73452	gbox159d08.x1 NCL_CGAP_Gas4 Homo sapiens	2.7
	407287	AI676812	Hs.167812	ESTs	2.7
	412797	AA125910	Hs.191461	six transmembrane epithelial antigen of t	2.7
	400298	AA032279	Hs.61635	FAT tumor suppressor (Drosophila) homolog	2.7
15	425483	AF231022	Hs.159159	equaporin 3	2.7
	430152	AB001325	Hs.234642	type 1 transmembrane protein Fn14	2.7
	444008	BE395085	Hs.10086	gbxq01d05.x1 Soares_NHCeC_cervical_tumor	2.7
	418859	AW516566	Hs.10086	fibrillin 2 (congenital contractual arac	2.6
	416658	U03272	Hs.79432	hypothetical protein DKFZp564A176	2.6
20	410290	AA042307	Hs.322844	a disintegrin and metalloproteinase doina	2.6
	419567	AU077005	Hs.92208	met proto-oncogene (hepatocyte growth fac	2.6
	406671	AA129547	Hs.285754	hypothetical protein MGC3295	2.6
	434444	A765276	Hs.101257	ATP-binding cassette, sub-family C (CFTR/	2.6
	421817	AF146074	Hs.108660	integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	431890	X17033	Hs.271986	Homo sapiens cDNA FLJ11041 1fs, clone PLA	2.6
25	452281	T93500	Hs.28792	thymidine kinase 1, soluble	2.6
	421608	BE302798	Hs.105087	ESTs	2.6
	453331	A1240665	Hs.8895	gbxy18601.s1 Soares placenta Nd2HP Homo	2.6
	447197	R38075	Hs.28075	Intercellular adhesion molecule 5, teloc	2.5
30	459688	UT2671	Hs.151250	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.5
	437412	BE069288	Hs.34744	DES1 protein	2.5
	429413	NM_014058	Hs.201677	prostaglandin E synthase	2.5
	424420	BE614743	Hs.146688	ubiquitin carrier protein	2.5
35	427239	BE270447	Hs.174070	hypothetical protein MGC13170	2.5
	407103	AA24881	Hs.256301	epididymis-specific, whey-acidic protein	2.5
	431130	NM_006103	Hs.2719	ESTs	2.5
	453379	AA035261	Hs.61753	fibroblast growth factor receptor 3 (echo	2.5
	421733	AL119871	Hs.1420	ESTs	2.5
	452220	BE158006	Hs.212298	hypothetical protein FLJ23186	2.5
40	417975	AA641838	Hs.30085	ESTs	2.5
	440381	AA917808	Hs.190495	ESTs	2.5
	441794	AW197794	Hs.253338	synaptophysin 3	2.5
	439108	AW163034	Hs.6467	C12001233.g1 7305361 refNP_038652.1 oto	2.4
	401103	NA	Hs.wwd	cystatin A (stefin A)	2.4
45	430630	AW269920	Hs.2621	hypothetical protein FLJ20401	2.4
	430129	BE301708	Hs.233955	ESTs	2.4
	416521	A1648602	Hs.55468	NM_002508:Homo sapiens nidogen (enactin)	2.4
	402745	D50915	Hs.38365	KIAA0125 gene product	2.4
50	457570	AA579428	Hs.208912	gbcmf37c09.s1 NCL_CGAP_Pr2 Homo sapiens c	2.4
	429574	BE268321	Hs.208912	hypothetical protein MGC851	2.4
	431211	M88949	Hs.323733	gap junction protein, beta 2, 26KD (come	2.4
	452865	A1924046	Hs.119567	ESTs, Weekly similar to A47562 B-cell gro	2.4
	420511	AF052692	Hs.58485	gap junction protein, beta 3, 31KD (come	2.4
55	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	2.4
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	418432	M14155	Hs.85112	insulin-like growth factor 1 (somatomedin	2.3
	438108	AI471795	Hs.287776	vanilloid receptor-related osmotically ac	2.3
	453408	AI192987	Hs.61784	hypothetical protein FLJ14451	2.3
60	435542	A1687376	Hs.288533	ESTs	2.3
	434517	A1635690	Hs.337251	hypothetical protein MGC2487	2.3
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	422310	AA316822	Hs.98370	cytochrome P450, subfamily IIb, polypepti	2.3
	441954	A7449395	Hs.8047	Fancn anemia, complementation group G	2.3
65	416091	AF295370	Hs.263082	defensin, beta 3	2.3
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-Ins	2.3
	409402	AF208234	Hs.595	cystatin B (stefin B)	2.3
	432284	AA532807	Hs.105822	ESTs	2.3
	408243	Y00787	Hs.624	interleukin 8	2.3
70	423229	AC039565	Hs.125532	protease, serine, 26	2.3
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohydri	2.3
	440502	AI624113	Hs.78281	regulator of G-protein signalling 12	2.3
	429929	AB014583	Hs.226275	KIAA0683 gene product	2.3
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolas	2.3
75	428953	AA306610	Hs.194676	tumor necrosis factor receptor superfamily	2.3
	438386	AA284267	Hs.221504	ESTs	2.2
	440371	BE288550	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
	452203	X67522	Hs.158164	transporter 1, ATP-binding cassette, sub-	2.2
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	2.2
80	432078	BE314877	Hs.24553	hypothetical protein FLJ12541 similar to	2.2
	429113	D28235	Hs.195384	prostaglandin-endoperoxide synthase 2 (pr	2.2
	452756	AW138937	Hs.213438	ESTs, Weekly similar to A34067 hypothetic	2.2
	428434	AW363390	Hs.65551	Homo sapiens, Similar to DNA segment, Chr	2.2
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.2

			lymphotoxin beta receptor (TNFR superfamily)	2.2	
			HCR (α -helix coiled-coil rod homologus)	2.2	
			immortalization-upregulated protein	2.2	
			phosphoribosyl/glycanamide formyltransferase	2.2	
			acetyl LDL receptor; SREC	2.2	
5	409994	D66864	TM,transSH2,SH3	5T4 oncofetal trophoblast glycoprotein	2.2
	417433	BE270268	SS,TM,LRRCT,LRRNT,LRR	solute carrier family 3 (activators of di	2.2
	416763	AI080127	TM,alpha-amylase7tm_1	ESTs, Weakly similar to I38022 hypothetical	2.2
	425999	AW513051	TM,FAD_binding_2,PS3PA,Ribosomal_S2,FAD_bind	ESTs	2.2
	452799	AI948829	TM	minichromosome maintenance deficient (S.	2.2
10	414733	BE514535	TM,MCMHeme_oxygenase	HMT1 (hnRNP methyltransferase, <i>S. cerevisiae</i>	2.2
	448153	Y10805	SS,TM,Na_Ca_Ex	artenin	2.2
	428999	AF120274	SS	TONDU	2.2
	443171	BE281128	SS,TM,7tm_1,nm	hypothetical protein DKF2p5640D0462	2.2
	408308	AL033377	TM,7tm_2	mitogen-activated protein kinase kinase k	2.2
15	409533	AWB69543	TM	hypothetical protein FLJ20561	2.1
	408201	AK000568	TM	glycoprotein (transmembrane) nmb	2.1
	408896	AI979168	TM	CDC20 (cell division cycle 20, <i>S. cerevisiae</i>	2.1
	417900	BE250127	TM,WD40,pro_isomerase	serine protease inhibitor, Kazal type, 5	2.1
	437191	NM_006846	SS,TM,kazal	Homo sapiens cDNA: FLJ23006 fs, clone LN	2.1
20	412834	R77123	TM,7tm_1	delta (Drosophila)-like 1	2.1
	431117	AF003522	SS,TM,DSL,EGF	cyclin-dependent kinase 2	2.1
	447874	BE270640	TM,pkinases,raf	FOS-like antigen-1	2.1
	409851	H96843	bZIPofflin_ADF,EGF	hypothetical protein DKFZp434I1930	2.1
25	440495	AA887212	TM,NSFNa_Ca_Ex	procollagen C-endopeptidase enhancer	2.1
	429415	NM_002593	HS202097	mutated in colorectal cancers	2.1
	421013	M62397	TM	protein tyrosine phosphatase, receptor ty	2.1
	447827	U73727	SS,TM,Y_phosphatase,fn3 Ig, MAM	hypothetical protein FLJ23399	2.1
	449224	AW995911	f63	transmembrane, prostate androgen induced	2.1
	452679	Z42387	TM	inhibin, beta A (activin A, activin AB al	2.1
30	409956	AW103364	He,727	ESTs	2.1
	438580	AA811262	TM,phasesesugar_Ir	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
	406400		SS,TM,trypsin	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
	424955	AW956282	He,144609	guanine nucleotide binding protein (G pro	2.1
35	412270	AC005262	TM,G-alpha	stratin	2.1
	428471	X57348	He,184510	metallocarboxypeptidase CPX-1	2.1
	427375	AL035460	He,177536	potassium channel, subfamily K, member 1	2.1
	416498	U33632	SS,Zn_carbOpept,hormone5Reprolysin	CG-09 protein	2.1
	423453	AW450737	He,79351	collagen, type V, alpha 2	2.1
40	417944	AU077198	He,82995	gem cell specific Y-box binding protein	2.1
	424197	AF096834	He,142889	prolactin receptor	2.1
	446163	AA026880	TM,25252	SHC (Src homology 2 domain-containing) tr	2.1
	417331	AW411297	He,81972	small inducible cytokine AS (RANTES)	2.1
	430413	AW842182	IL8,PX	ATPase, Ca transporting, type 2C, member	2.1
45	421685	AF189723	He,106778	gb:av35f03.r1 NCI_CGAP_Bi5 Homo sapiens c	2.1
	407305	AA716284	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	putative secreted ligand homologous to f]	2.0
	407792	AI077715	He,39384	hypothetical protein MGC2991	2.0
	418695	AA447014	SS	sema domain, immunoglobulin domain (Ig),	2.0
	439736	BE246502	SS	ESTs	2.0
50	433398	AW843150	TM,ResGAP,IQ,VW	ESTs .	2.0
	455327	H68741	He,112412	pymidinergic receptor P2Y, G-protein co	2.0
	446872	X97058	TM,Glyco_transf_8	bone morphogenetic protein 1	2.0
	419726	U50330	He,1274	squamous cell carcinoma antigen recognize	2.0
	410116	AW630671	He,58636	KIAA0450 gene product	2.0
55	426500	NM_014638	He,170156	olfactory receptor, family 2, subfamily I	2.0
	452194	AI684413	He,332649	microfibrillar-associated protein 2	2.0
	418140	BE613836	He,83551	kalikrein 12	2.0
	425856	AF135025	He,159679	ESTs	2.0
	434346	AA630445	He,116773	tumor necrosis factor (ligand) superfamily	2.0
	426274	D38122	He,2007	ESTs	2.0
60	440008	AW051683	He,276566	cartilage intermediate layer protein, nuc	2.0
	424634	NM_003613	He,151407	Homo sapiens mRNA; cDNA DKFZp564O1016 (fr	2.0
	446841	AI049229	ig,lsp_1	ESTs	2.0
	418851	AI417828	He,192435	RAD1 (<i>S. pombe</i>) homolog	2.0
65	440351	AF030933	He,7179	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	439498	BE816501	He,32343	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	454197	BE140986	TM,Ammonium_transpkinase,Ammonium_transp	cadherin, EGF LAG seven-pass G-type recep	2.0
	433573	AF234887	He,57652	gap junction protein, beta 6 (connexin 31)	2.0
	429211	AF052693	He,198249	tumor necrosis factor (ligand) superfamily	2.0
	420737	L08098	He,99899	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
70	455333	AW897851	TM,Glyco_hydro_2	survival of motor neuron 1, telomeric	2.0
	414784	NM_000344	He,288966	homolog of yeast long chain polyunsaturat	2.0
	435836	AW292532	SS,TM,BIR	DKFZP564I1922 protein	2.0
	411789	AF245505	TM,GNS1_SUR4	zinc-finger regulated transporter-like	2.0
	441455	AJ271671	TM,gLRRC1	Jagged 2	2.0
75	426068	AF029778	He,166154	hypothetical protein from EUROIMAGE 17593	2.0
	437333	AL365412	TM,Sm	mitochondrial ribosomal protein L17	1.9
	435014	BE660898	He,10026	ESTs, Highly similar to unnamed protein p	1.9
	457819	AA057484	He,35406	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
	422737	M26939	He,119571	ESTs	1.9
80	431104	AW970859	He,313503	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	432210	AI567421	He,273330	ESTs	1.9
	436511	AA721252	He,291502	small inducible cytokine subfamily B (Cys	1.9
	419218	AU076718	He,164021		

				TM,Pribosyltran		
432169	Y00971	Hs.2910		TM,ras		
441128	AA570256	Hs.54628		TM		
447160	AA330310	Hs.24181		TM,RYDR_JTPR,RyR,SPRY		
419138	U49508	Hs.89631		TM,hemopexin_Peptidase_M10		
5	457817	AA247751	Hs.79572	TM,connexin		
	431009	BE149762	Hs.48956	SS,TM,connexin		
	428957	NM_003881	Hs.194679	SS,TM,wwo_1GFBP,isp_1		
	418546	AA224827		TM,wwo_1GFBP,isp_1		
10	400749			TM,wo_1GFBP,isp_1		
	408369	R38438	Hs.182575	F-protein		
	422765	AW409701	Hs.1578	TM,B1R		
	417409	BE272506	Hs.2109	TM,Syndecan		
	407720	AB037776	Hs.38002	TM,calponin,CH		
15	418830	AA157371	Hs.88959	TM,CDP-DH_P_transf,MCM		
	434769	AA648884	Hs.134278	TM,CDP-DH_P_transf,MCM		
	421593	NM_017436	Hs.105956	SS,TM		
	426064	BE387014	Hs.166146	TM,WH1		
	404604	NA		TM		
20	422753	A1928995	Hs.1575	SS,TM,Sm		
	422739	H20106	Hs.119591	SS,Cla_adaptor_s		
	433068	NM_006456	Hs.288215	SS,Pribosyltran		
	418594	AA013051	Hs.91417	TM		
	428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core		
	428343	AL043021	Hs.12705	TM,Ribomboid,HMG_boxTPR		
25	429592	AB029041	Hs.209546	Tropolin		
	431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2		
	424870	W61215	Hs.116651	tg		
	428373	A1751656	Hs.183966	SS,TM,g		
	453449	W16752	Hs.32981	SS,tg,Sema		
30	432304	AA932186	Hs.69297	TM,7tm_1		
	432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_CDnaJ		
	416207	NM_014745	Hs.338433	SS,TM_zf-DHMC		
	408988	AL119844	Hs.49476	TM,PlxIn_repeat,Bemta_tsp_1		
	417426	NM_002291	Hs.82124	SS,lamlin_EGF_lamlin_Nterm		
35	443863	AA114212	Hs.9930	SS,TM,serpin,Marek_A		
	433328	AW298159	Hs.23644	SS,TM		
	418981	AA897581	Hs.128773	TM,S14_Sno		
	420931	AF044197	Hs.100431	SS,TM,JB		
40	415023	AA932146	Hs.133494	TM,Ribosomal_S17Ribosomal_L13		
	413644	BE154910	Hs.278793	TM,Glyco_hydro_2		
	449987	AW079749	Hs.164719	TM,ABC_tran,ABC_membrane,ton_trans		
	421340	F07783	Hs.1369	SS,sushi		
	417886	AW067903	Hs.82773	SS,TM,Collegen,COLFI,TSPN		
	430259	BE550182	Hs.127826	TM,transmembrane4RaGEF,RA		
45	432998	AA835948	Hs.153307	TM,SDF		
	431671	NM_016937	Hs.267289	TM,NA		
	411773	NM_005799	Hs.72026	trypsin		
	425247	NM_005940	Hs.155324	SS,TM,Peptidase_M10,hemopexin		
	422976	AU076657	Hs.1600	TM,cpn60_TCP1,Sema		
50	425169	NM_004341	Hs.154686	SS,TM,GTase,OTCace,CPSase_I_chain,Dihydrooro		
	447776	AI526525	Hs.130181	Rho_B_leucin		
	426908	AW8415163	Hs.172851	SS,TM,fusion_gly_Myosin_tailoch_short		
	408116	AA251393	Hs.289052	TM,Mn_Ca_ExCam_acyltransf		
	417847	AI521658	Hs.7331	Uteroglobin		
	415781	H08368	Hs.78853	SS,TM,UNG		
	407903	AI287341	Hs.154029	TM,ubiquitin_lammin_G_lammin_EGF_kazal		
	422511	AI076442	Hs.117938	TM,p450		
	414117	W88559	Hs.1787	TM,Ion_trans,K_tetra		
60	426841	AI052358	Hs.193726	TM,asp		
	415272	AA164215	Hs.203188	TM,TPR,pkinase,lg,B56		
	426440	BE382756	Hs.168902	TM,sugar_Ir,Fork_head		
	419488	AA316241	Hs.90691	FCF		
	418452	BE379749	Hs.85201	SS,TM,leclin_C		
65	431363	M86528	Hs.266902	SS,NGF		
	440975	AW499914	Hs.7579	SS,TM		
	438962	BE046894	Hs.296585	TGF-beta,bZIP		
	414602	AW630088	Hs.76550	SS		
	418054	NM_002318	Hs.83364	TM,mito_carr,Lysyl_oxidase		
	440501	AA887391	Hs.202229	TM,Galactosyl_T		
70	449309	AW589823	Hs.224189	TM		
	421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7		
	412584	X54870	Hs.74085	TM,leclin_c		
	441565	AW953575	Hs.303125	TM		
	431837	T79328	Hs.328553	TM,7tm_3,ANF_receptor,sushi		
75	436251	BE516065	Hs.296585	SS,Y_phosphataseTIG		
	448833	AA311426	Hs.21635	TM,EGF_lammin_G_fibrinogen_C,F5_F8_type_C,tubulin		
	424291	AL120051	Hs.144700	TM,Ephrin_HisL_deacetyl		
	415388	AF018881	Hs.78409	SS,TM,TSPN,Collagen		
	435550	A1224456	Hs.4934	TM,LRR,LRRCT		
80	448568	AA149121	Hs.71947	TM,LRRCT		
	439246	AI498072	Hs.77783	SS,TM,REJ_PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla		
	410001	AB041036	Hs.57771	SS,TM,trypsin		
	417312	AW888411	Hs.81915	SS,Slahmin		
				phosphonibosyl pyrophosphate synthetase 2	1.9	
				ESTs, Weakly similar to T23273 hypothetical	1.9	
				ESTs	1.9	
				ryanodine receptor 1 (skeletal)	1.9	
				cathepsin D (lysosomal aspartyl protease)	1.9	
				gap junction protein, beta 5 (connexin 30)	1.9	
				WNT1 inducible signaling pathway protein	1.9	
				gb:nc032g04.s1 NCI_CGAP_Pr2 Homo sapiens c	1.9	
				NM_003105 Homo sapiens sortilin-related	1.9	
				solute carrier family 16 (H???) transports	1.9	
				baculovirus IAP repeat-containing 5 (surv	1.9	
				syndecan 1	1.9	
				KIAA1355 protein	1.9	
				hypothetical protein MGC4B16	1.9	
				Homo sapiens cDNA FLJ12576 fs, clone NT2	1.9	
				globotriacylceramide/CD77 synthase; Gb3/	1.9	
				Homer, neuronal immediate early gene, 3	1.9	
				Target_Exon	1.9	
				small nuclear ribonucleoprotein D3 polype	1.9	
				adaptor-related protein complex 2, sigma	1.9	
				slalyltransferase	1.9	
				topoisomerase (DNA) II binding protein	1.9	
				transglutaminase 1 (K polypeptide epiderm	1.9	
				ESTs	1.9	
				KIAA1118 protein	1.9	
				2-S-oligoadenylate synthetase 2 (69-71	1.9	
				epithelial V-like antigen 1	1.9	
				poliovirus receptor-related 2 (herpesvirus	1.9	
				sema domain, immunoglobulin domain (Ig).	1.9	
				ESTs	1.9	
				DnaJ (Hsp40) homolog, subfamily B, member	1.9	
				Homo sapiens, clone MGC:2908, mRNA, comp	1.9	
				Homo sapiens clone TUAB_Ct1-du-chat regio	1.9	
				laminin, beta 1	1.9	
				serine (or cysteine) proteinase inhibitor	1.9	
				ESTs, Weakly similar to S65B24 reverse lr	1.9	
				ESTs	1.9	
				small inducible cytokine B subfamily (Cys	1.8	
				Homo sapiens clone Z195_JUMAN_ZINC F	1.8	
				ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8	
				decay accelerating factor for complement	1.8	
				collagen, type XI, alpha 1	1.8	
				RelGEF-like protein 3, mouse homolog	1.8	
				ESTs	1.8	
				polymerase (DNA directed), alpha	1.8	
				protease, serina, 21 (testis)	1.8	
				matrix metalloproteinase 11 (stromelysin)	1.8	
				chaperonin containing TCP1, subunit 5 (cp	1.8	
				carbamoyl-phosphate synthetase 2, aspara	1.8	
				NDP-N-acetyl-alpha-D-galactosaminopolype	1.8	
				angiase, type II	1.8	
				Homo sapiens, Similar to RIKEN cDNA 54304	1.8	
				hypothetical protein FLJ22216	1.8	
				uracil-DNA glycosylase	1.8	
				bHLH factor Hes4	1.8	
				collagen, type XVII, alpha 1	1.8	
				proteolipid protein 1 (Pelizaeus-Merzbach	1.8	
				ESTs	1.8	
				ESTs	1.8	
				solute carrier family 2 (facilitated gluc	1.8	
				nucleophosphom/nucleoplasmn 3	1.8	
				C-type (calcium dependent, carbohydrate-r	1.8	
				neurotrophin 5 (neurotrophin 4b)	1.8	
				hypothetical protein FLJ10402	1.8	
				gbdbn4ic11.x1 NCI_CGAP_RDF2 Homo sapiens	1.8	
				Homo sapiens mRNA; cDNA DKFZp564B1264 (fr	1.8	
				lysyl oxidase-like 2	1.8	
				ESTs	1.8	
				ESTs	1.8	
				ESTs, Weakly similar to A45010 X-linked r	1.8	
				DNA segment on chromosome 12 (unique) 24B	1.8	
				p53-induced protein PIGPC1	1.8	
				olfactory receptor, family 2, subfamily 1	1.8	
				nucleolar protein [KREU repeat]	1.8	
				tubulin, gamma 1	1.8	
				epilin-B1	1.8	
				collagen, type XVIII, alpha 1	1.8	
				H.sapiens polyA site DNA	1.8	
				ESTs	1.8	
				membrane-associated tyrosine- and threonin	1.8	
				kalikrein 11	1.8	
				leukemia-associated phosphoprotein p18 (s	1.8	

				hypothetical protein MGC2803	1.8
				PRP4/STK/WD_splicing factor	1.8
				Cip1-interacting zinc finger protein	1.8
				ESTs, Moderately similar to R27328_2 [Hs]	1.8
				DNA segment on chromosome 19 (unique) 117	1.8
5	444152	AJ125694	Hs.149305	TM	
	453454	AW052006	Hs.8551	TM	
	449320	AB030835	Hs.23476	SS,adenylatekinase	
	428329	AA226091	Hs.98453	TM,Gal-bind_Jecin	
	452875	BE275760	Hs.30928	TM,Apolipoprotein	
	444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	
	443534	AJ078123		TM	
	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7m_2	
10	452874	AK001061	Hs.30925	SS	
	453140	AA032238	Hs.170531	TM	
	416641	BE243136	Hs.85947	SS,TM,disintegrin,Pep_M12B_propep,Reprolysin	
	432925	AA878324	Hs.192734	SS	
	453857	AT080235	Hs.35881	TM	
	457663	AN371946	Hs.337459	TM	
15	452873	AK001247	Hs.30922	TM	
	436396	AI6B3487	Hs.152213	SS,wnt	
	452835	AK001269	Hs.30738	TM	
	459647	R34107	Hs.198287	ig	
20	418245	AA088767	Hs.83883	TM,PEPCK	
	448484	BE613340	Hs.334725	TM	
	431369	BE184455	Hs.251754	SS,wap	
	434877	AW974792	Hs.292171	TM	
	428923	BE047698	Hs.188785	TM	
25	402915	NA		TM,HCO3_cobransp	
	420185	AL044056	Hs.158047	TM	
	445739	AW136354	Hs.145303	TM	
	408435	AI810721	Hs.95424	TM,p450	
	406688	AI634522	Hs.152925	TM	
30	420085	AI741909	Hs.44680	TM	
	433933	AI754389	Hs.133494	TM,Ribosomal_S17/Ribosomal_L13	
	430965	AA468732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_YDP	
	423484	NM_016240	Hs.128856	TM,Collagen	
35	416737	AF154335	Hs.79891	SS,TM,LIM,PDZsugar_Ir,PDZ,LIM	
	409012	AL117435	Hs.49725	TM,RicGEFz7-DHHC,adh_short	
	423804	AW034448	Hs.1705	TM,IRF	
	410418	D31382	Hs.63325	SS,TM,trypsin,kl_recept_a	
	440028	AW747675	Hs.125843	TM	
40	457646	AAT28560	Hs.112948	TM,SPRY	
	445439	BE243084	Hs.12719	SS,TGF-beta	
	420426	AA262045	Hs.36567	TM,Galactosyl_T,2ATP-synt_C	
	431341	AA307211	Hs.251531	TM,proteasome	
	412338	AA151527	Hs.68485	TM,Serine_Plexin_repeatTIG,Plexin_repeat	
45	414799	AT752416	Hs.77326	SS,thyroglobulin_I,GFBP	
	452700	AI859390	Hs.288940	TM,DIX,RGS,flored	
	430877	NM_005269	Hs.2693	GST_C,IRNA-synth_1,WHEP-TRS,TGF-beta	
	428624	AI125222	Hs.98712	TM,thiore_I,Y_phosphatase,MAM,tg,fn3MSP_domain	
	444065	AW449415	Hs.10260	TM,ion_trans	
50	416319	AI816801	Hs.79197	SS,TM/tg	
	429367	AB007867	Hs.278311	Serine_Plexin_repeat,TIG	
	430425	AA631428	Hs.241412	TM	
	441668	A611973	Hs.127525	TM,Ammonium_bansp	
	418469	U34879	Hs.85279	SS,TM,edh_short	
55	450035	BE262773	Hs.25584	TM,ArfGap	
	418859	AA229558		TM	
	425304	AA465844	Hs.31339	TM,g,ITAM	
	423635	X85019	Hs.130181	TM,Rho_B_Jecin	
	414820	AA371931	Hs.77422	TM,ion_trans,LIM,Synaptophysin	
60	440654	AW014242	Hs.159998	TM,connexin	
	412276	BE262621	Hs.73798	SS,MIF	
	422087	X58968	Hs.111301	SS,Peptidase_M10,fn2,hemopexin	
	407151	H26836	Hs.301527	SS,TNF	
	410726	AI822859	Hs.15936	TM,PX	
65	452012	AA387703	Hs.279766	TM,kinesin	
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	
	409220	BE243323	Hs.51233	TM,death,TNFR_c6	
	427082	AB037850	Hs.173484	TM,mbo_carr	
	426410	BE298446	Hs.305890	TM,Bcl-2,BH4	
70	433598	AT762636	Hs.271433	TM,Cytidylyltrans,SIR27tm_2	
	436495	BE258949	Hs.290874	TM,Annmedillo_seg	
	422032	AA473986	Hs.110857	TM,TFIIS,RNA_POL_M_15KDserpin,hormone_rec,zf-C4	
	429736	AF125304	Hs.212680	SS,TNFR_c6	
	427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	
75	431981	AA684069	Hs.115779	Iammin_B,Iammin_EGF	
	407736	N41744	Hs.19976	TM,Sulfatase	
	420187	AK001714	Hs.95744	TM	
	424620	AA101043	Hs.161254	SS,TM,trypsin	
	430488	D19589	Hs.13453	TM	
80	423393	R37772	Hs.21420	TM,ubcirepkhnase	
	444051	N48373	Hs.10247	SS,jg	

TABLE 13B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT Number	Accessions
10	408344	105240_1	AA053843 BE162213
	418546	175677_1	AA224827 T59706 T59843 BE158903
	418659	179717_1	AA229558 AA345492 AA229582
	418669	179863_1	AW516565 AA229762 AA23035
15	437938	44573_2	AJ950087 N70208 R97040 N365809 AJ0308119 AW967677 N35320 BE151473 H59397 AW971573 R97278 W01059 AW967671 AA808598 AA251875 AJ820501 AJ820532 W87891 T85904 U71456 BE328571 T75102 R34725 AA884922 BE328517 AJ219788 AA884444 N92578 F13493 AA927784 AJ560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AJ890387 AJ950344 AJ741345 AJ689062 AA282915 AW102898 AJ872183 AJ763273 AW173586 AW160329 AJ653832 AJ762688 AA988777 AA488892 AJ366394 AW103813 AJ539642 AA642789 AA856975 AW505512 AJ961530 AW629970 BE612891 AW276997 AW613601 AW512843 AA044208 AW856538 AA180009 AA337499 AW981201 AJ251669 AA251874 AJ819225 AW205862 AJ683338 AJ858509 AW276905 AJ633006 AA972584 AA988741 AW072629 AW513996 AA283273 AA969759 N76828 N22388 H84729 H80052 T92497 AJ022058 AA780419 AA551005 W80701 AW613456 AJ373032 AJ564269 F00531
	438852	467390_1	BE046894 BE046667 AA828585 AJ207343
	443534	572957_1	AI076123 AJ244834 AJ695239
	447197	711623_1	R36075 AJ366546 R36167
20	454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141659 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141650 BE141688 AW178241 BE140994 BE141666 BE140988 BE141008 BE140988 BE141011 BE140975 BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140980 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141645 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141002 BE141566
	455333	1281044_1	AW897851 AW897652
	457570	357443_1	AA579426 AA579436 AA573736

TABLE 13C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., *Nature* (1999) 402:489-495.

40 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
45	400666	8118496	Plus	17982-18115,20297-20456
	400749	7331445	Minus	9162-9293
	401103	8568122	Minus	98330-98449
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
50	401575	7229804	Minus	76253-76364
	402745	9212200	Minus	76516-76690
	402915	7406502	Minus	140-276
	404440	7528051	Plus	80430-81581
	404604	9212537	Minus	72019-72509
55	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	406400	9256208	Plus	1653-1712,1876-2140,4252-4385,5922-6077
	408467	8785551	Plus	182212-182958

60

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

65 Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. kinase, peptidase, phosphatase, ATPase, or ion_transporter domains). The predicted protein domains are noted.

70 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	PPDomains	Unigene Title	R1
80	418007	M13509	Hs.83169	SS_hemopexin_Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
	438506	W79123	Hs.58561	TM_7m_1	G protein-coupled receptor 87	28.8
	400289	X07820	Hs.2258	hemopexin_Peptidase_M10	matrix metalloproteinase 10 (stromal)	20.5
	415817	U88957	Hs.78867	SS_TM_Y_phosphatase_carb_enhyd	protein tyrosine phosphatase, receptor	16.4
	416209	AA235776	Hs.79078	TM_HORMA	MAO2 (mitotic arrest deficient, yeast)	15.4
	404996	NM_001333	Hs.87417	Peptidase_C1	CTS2 Cathepsin L2	13.1

				Target CAT	
5	428618	AA885360	Hs.160199	phosphatase	12.7
	429486	AF155827	Hs.203963	heparanase_C,SNF2_Nheparanase_C	12.6
	419183	U60669	Hs.89663	p450	12.3
	428368	BE440042	Hs.83326	SS_Peptidase_M10_hemopexin	10.2
10	420759	T11832	Hs.127797	heparanase_C	10.2
	458194	AW383618	Hs.265459	p450	9.4
	446232	AI281848	Hs.194691	TM_7tm_3Ribosomal_L13	8.9
	424905	NM_002497	Hs.153704	TM_phosphatase	8.9
15	452291	AF015592	Hs.28853	TM_phosphatase	8.7
	424086	A1351010	Hs.102267	Lysyl_oxidase	8.3
	425716	AF030880	Hs.159275	TM_Sulfate_transp_STAS	7.8
	433133	AB027249	Hs.104741	TM_Collagen_phosphatase	7.4
	447254	NM_004153	Hs.17908	SS_AAA_BAH	7.1
20	431941	AK000106	Hs.272227	peptidase_Furin-like_Recap_L_dom	6.9
	427821	AA470158	Hs.98202	TM_7tm_1	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	6.9
	403471	NA		SS_TM_trypsin	6.7
	410153	BE311926	Hs.15830	Glycos_transf_2	6.5
25	457405	AA504860	Hs.242998	TM_7tm_2	6.4
	421948	LA2583	Hs.334309	filamentousHCO3_cotransfilament	6.3
	439292	AA090421	Hs.5555	TM_AAA_Ferric_reduct	5.8
	413625	AW451103	Hs.71371	TM_E1-E2_ATPase_Hydrolase	5.8
	425685	NM_005401	Hs.159238	TM_Band_41_Y_phosphatase	5.8
	438394	BE379823	Hs.27693	SS_pro_isomerase	5.6
30	432239	X81334	Hs.2936	SS_Peptidase_M10_hemopexin	5.5
	408536	AW381532	Hs.135188	SS_TM_E1-E2_ATPase_Cathepsin_ATPase	5.5
	432225	AW182766	Hs.273558	Cytidylyltransf	5.4
	419520	AB009303	Hs.90800	TM_hemopexin_Peptidase_M10	5.2
	426360	NM_003245	Hs.2022	TM_Transglutaminin_C_Transglutamin	5.1
	421155	H87879	Hs.102267	SS_Lysyl_oxidase_Aldose_epimerase	5.0
	423673	BE003054	Hs.1695	SS_TM_Peptidase_M10_hemopexin	4.9
	450375	AA009647	Hs.8850	TM_disintegrin_Pep_M12B_propep	4.8
	418379	AA218940	Hs.137516	AAA	4.7
35	457465	AW301344	Hs.128908	Prbonyltran_Sulfatase	4.6
	412333	AW937485	Hs.242998	TM_7tm_3	4.6
	450510	AA010066	Hs.5101	DNA_topoisom_DNA_topoisom_VtGF	4.6
	436291	BE568452	Hs.5101	abhydrolase	4.6
	448363	A1290919	Hs.353661	HECT_phosphatase	4.5
40	435435	T89473	Hs.192328	lipase_PLAT	4.5
	425071	NM_013969	Hs.154424	SS_TM_T4_deiodinase	4.4
	433222	H50621	Hs.134156	TM_Ion_trans-BN-ARC_CARD_mito_c	4.4
	408908	BE296227	Hs.250822	TM_phosphatase	4.4
	444781	NM_014400	Hs.11950	PH_fadulase_B	4.4
45	428479	Y00272	Hs.184572	plkinase	4.2
	406687	M31126	Hs.272620	SS_Peptidase_M10_hemopexin	4.2
	423035	AW448679	Hs.156739	TM_Glyco_Isoflg_B	4.2
	449228	AA403107	Hs.148590	TM_PAF-AH_p450	4.2
	423738	AB002134	Hs.132195	SS_TM_trypsin_SEA	4.1
	457030	AI301740	Hs.173381	TM_Dihydroorotate	4.1
50	448995	AB613276	Hs.5662	adenylatekinase	4.0
	415857	AA866115	Hs.127797	heparanase_C	4.0
	438390	AI422017	Hs.30875	TM_DSL_7tm_17tm_1	4.0
	429900	AA460421	Hs.30875	phosphatase	4.0
55	446292	AF081497	Hs.278682	Ammonium_transp	3.8
	422938	NM_001809	Hs.1594	TM_biolase	3.7
	408771	AW732573	Hs.47584	TM_K_tetra_Ion_trans	3.6
	424286	AW631674	Hs.165140	plkinase	3.6
	436246	AW450963	Hs.119991	conexinhomone_rec_zf-C4	3.5
60	411274	NM_002776	Hs.69423	tryptin	3.5
	400666			SS_hemopexin_Peptidase_M10	3.5
	426920	AA383351	Hs.132121	PDEase	3.5
	412471	M63193	Hs.73946	SS_TM_Glycos_transf_3_Cam_acy	3.4
	430704	AW813091	Hs.335799	Epimerase	3.4
65	455092	BE152428		Sulfatase	3.4
	453775	NM_002916	Hs.35120	AAA_PI3_Pi4_kinase_PI3Ka_PI3K_	3.4
	438993	AAB28995		Integrin_B	3.4
	426572	AB037783	Hs.170623	hormone_rec_zf-C4	3.4
	449101	AA205847	Hs.23018	SS_TM_7tm_1	3.3
	427680	AI741320	Hs.114121	hormone_rec_zf-C4	3.3
70	402481			TM_GDI_7tm_1	3.3
	414774	X02419	Hs.77274	SS_kinase_trypsin	3.3
	412246	AI160873	Hs.59233	SulfotransferaseACOX	3.3
	418462	BE001596	Hs.85266	SS_TM_Integrin_B_fn3	3.3
	424687	J05070	Hs.151738	SS_Peptidase_M10_fn2_hemopexin	3.3
75	401486	NA		SS_TM_trypsin	3.2
	408113	T82427	Hs.194101	TM_7tm_3Ribosomal_L13	3.2
	427359	AW020782	Hs.79881	TM_7tm_1	3.2
	402337			SS_p450	3.2
80	420930	AW868650		ribonuclease_T2	3.2
	443426	AF098158	Hs.9329	phosphatase	3.1
	439760	AL359063	Hs.57664	TM_Integrin_B_Ricin_B_lecithin	3.1
	420039	NM_004605	Hs.94581	CARD_SulfotransferDAGKc	3.0
	448733	NM_005629	Hs.187958	SS_TM_SNFRABC Tran_isodhn_pkina	3.0

				SS, TM, abhydrolase	hypothetical protein FLJ2240B	3.0
				pro_isomerase	ESTs	3.0
				death_pkinese	biphenyl hydrolase-like (serine hyd)	3.0
				pkinese	gbac50c03.s1 Stratagene hNT neuron	2.9
				TM, p450	ESTs, Weakly similar to fatty acid	2.9
5	446733	AA863360	Hs.26040	SS, TM, lipoxygenase,PLAT	ESTs, Weakly similar to CP4Y_HUMAN	2.9
	449746	AI688594	Hs.178588	SS,p450	arachidonate 12-lipoxygenase	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	ESTs	2.9
	414581	AA256213	Hs.72010	TM,Carn_acyltransf,Choline_kin	interferon, alpha-inducible protein	2.8
10	431629	AU077025	Hs.265827	SS, tRNA_antith2,S13, pkinese	poly(A)-binding protein, cytoplasmic	2.8
	445873	AA260970	Hs.251946	SS,rrn,PABPpknhase,14-3-3,rrn	ESTs	2.8
	438113	AI67908	Hs.3882	TM,7m_1	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
	422689	AW856565		helicase_C,SNF2_Nhelicase_C	thyroid hormone receptor Interactor	2.8
	439453	BE264974	Hs.6566	SS,AAA	hypothetical protein MGC5350	2.8
15	413582	AV295847	Hs.71331	carb_anhydrase	lipase, endothelial	2.8
	410684	NM_006033	Hs.65370	TM,lipase,PLAT	nuclear cap binding protein subunit	2.8
	456456	AA477609	Hs.89583	FBPase	stem-loop (histone) binding protein	2.8
	413273	U75579	Hs.75257	TM,lg_pkinese	KIAA0035 gene product	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7m_1	NM_0010597:Homo sapiens tachykinin	2.7
20	403783			TM,7m_1	dubiquitin	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7m_3,ANF_receptor	NM_014191*:Homo sapiens sodium chan	2.7
	401230			SS,TM,ion_trans,IQ	neurominic B	2.7
	418030	BE207673	Hs.83321	SS,TM,Peptidase_S28,Bombesin	ESTs, Weakly similar to KIAA0227 [H]	2.7
	445640	AW969626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to I3022 hypo	2.6
25	432865	AT753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	a disintegrin and metalloproteinase	2.6
	419667	AU077005	Hs.92208	SS, TM,disintegrin,Regrilosin,P	met proto-oncogene (hepatocyte grow	2.6
	406671	AA129547	Hs.285754	TM, pkinese,Plexin_repeat,Sema,	hypothetical protein FLJ13346	2.6
	412530	AA766268	Hs.256273	abhydrolase	Inegrin, alpha 2 (CD49b), alpha 2 s	2.6
	431890	X17033	Hs.271986	vwa,FG-GAP,Integrin_A	NM_030903*:Homo sapiens olfactory r	2.6
30	404184	NA		SS,TM,7m_1	KIAA0175 gene product	2.6
	428450	NM_014791	Hs.184339	pidase,KA1	polycystic kidney disease 2-like 1	2.6
	425698	NM_016112	Hs.159241	TM, pkinese,ion_trans	ESTs	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
	444826	AI674482	Hs.148441	pkinese,SAM	hypothetical protein FLJ14950	2.6
35	414987	AA524394	Hs.294022	converininome_ec,zf-C4,com	ESTs	2.5
	438745	AI685815	Hs.184727	Ribosomal_S2,transferrin	DESC1 protein	2.5
	429413	NM_014058	Hs.201877	trypsin	hypothetical protein MGC13170	2.5
	407103	AA424881	Hs.256301	TM, cNMP_bindingtrypsin	ESTs	2.5
	453379	AA035261	Hs.81753	PAN_kringle,lypsin	fibroblast growth factor receptor 3	2.5
40	421733	AL119671	Hs.1420	SS,TM,lg_pkinese	ESTs	2.5
	452220	BE158006	Hs.212298	TM, integrin_A,FG-GAP	hypothetical protein FLJ23186	2.5
	417975	AA641836	Hs.30085	SS, trypsin	estrogen receptor 1	2.5
	400301	XJ3635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	ESTs	2.4
	408938	AA059013	Hs.22607	Y_phosphatase	hypothetical protein FLJ22028	2.4
45	411843	AI924519	Hs.192570	DEAD, helicase_C	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
	446638	AI133063	Hs.15783	TM, pkinese	hypothetical protein FLJ20401	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ14813	2.4
	417655	AA780791	Hs.14014	Peptidase_M41,AAPknhase	ESTs	2.4
	448005	AW207437	Hs.170378	pkinese	arachidonate 12-lipoxygenase, 12R I	2.4
50	423973	AF038481	Hs.136574	SS, pro_isomerase	hypothetical protein FLJ22869	2.4
	437897	AA770561	Hs.146170	DNA_topoisolDNA_topoisolVIGF	topoisomerase (DNA) II alpha (170kD)	2.4
	423937	J04688	Hs.156346	alpha_amylase	ESTs	2.4
	432777	AA564991	Hs.269477	TM,IRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
55	421247	BE391727	Hs.102910	TM,pkinese,DAG_PE-bind,OPR,old	protein Kinase C, Iota	2.4
	425465	L18964	Hs.1904	TM,E1-E2_ATPase,HMA,Hydrofase	ESTs	2.4
	419281	H96452	Hs.42189	SII3,eflend,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
	434205	AF119851	Hs.283032	phosphatase,Furin-like,Recep_L-dom	hypothetical protein FLJ14451	2.3
	453406	AI192967	Hs.81784	phosphatase,RhoGEF,jg,PH,SH3	ESTs	2.3
	435542	AA687378	Hs.269533	TM,132714	integrin, alpha 3 (antigen CD48C, a	2.3
60	443151	AI827193	Hs.265829	SS, TM,FG-GAP,Integrin_A	cytochrome P450, subfamily 1I5, pol	2.3
	431630	NM_002204	Hs.265829	SS, TM,fn3,lg_pkinese, Ribosomal	Fanci anemia, complementation gro	2.3
	422310	AA316622	Hs.98370	alpha_amylase	polo (Drosophila)-like kinase	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	EST	2.3
	414907	X00725	Hs.77597	SS, TM, pkinese,POLO_box	matrix metalloproteinase 14 (membra	2.3
	439810	AL109710	Hs.865658	aconitase,Aconitase_C	ESTs	2.3
	429359	W00482	Hs.2399	SS, TM,Peptidase_M10,hemopexin	gbad50f04.x1 NCI_CCAP_Gas4 Homo sa	2.3
	432284	AA532807	Hs.105822	TM, pkinese	protease, serine, 26	2.3
65	452847	AW130413	Hs.125532	alpha_amylase	Bloom syndrome	2.3
	423229	AC003865	Hs.125532	SS,trypsin	platelet-activating factor acetylhy	2.3
	453841	U99817	Hs.36820	DEAD,HRDC,helicase_C	Igase I, DNA, ATP-dependent	2.2
70	439563	AW247529	Hs.6793	TM,p450Ets	ESTs, Weakly similar to A34087 hypo	2.2
	424439	AA579635	Hs.1770	DNA_ligase	H1 histone family, member 0	2.2
	452765	AW138937	Hs.213436	Glyco_transf_29	hypothetical protein MGC5469	2.2
	428922	Z97630	Hs.226117	TM,linker_histone7tm_1	phosphoribosylglycanamide formyltra	2.2
	434149	Z43829	Hs.19574	TM,EPH_Ibd,fn3, pkinese,SAM	acetyl LDL receptor, SREC	2.2
75	417576	AA339449	Hs.82285	TM,APB,formyl_transf,GARS	solute carrier family 3 (activators	2.2
	409994	D86864	Hs.57735	IP_ltransSH2,SH3	microchromosome maintenance deficien	2.2
	416763	AI906127	Hs.79748	TM, alpha_amylase7tm_1	TONDU	2.2
	414733	BE514535	Hs.77171	TM,MCM4/heme_oxygenase	S100 calcium-binding protein A11 (c	2.2
	443171	BE281128	Hs.9030	SS,TM,7m_1,mm	eyes absent (Drosophila) homolog 2	2.2
80	430637	BE160081	Hs.255290	S_100Peptidase_M16	hypothetical protein DKFZp564D0462	2.2
	452367	U71207	Hs.29279	SS,Hydrolase	CDC20 (cell division cycle 20, S. c	2.2
	408308	AL033377	Hs.44197	TM,7m_2		2.1
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase		

	424490	AJ278016	Hs.55565	TM_pkinase_ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM_7m_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N_helicase_C	RAD64 (S.cerevisiae)-like	2.1
5	418804	AA809632		HATPase_c_HSP90,PHD_zf-C2H2	glnz17h04.s1 NCL_CGAP_GCB1 Homo sa	2.1
	47674	BE270640	Hs.19192	TM_pkinase_sf	cyclin-dependent kinase 2	2.1
	450563	H43540	Hs.25292	SS_TM_RNase_HII	ribonuclease HI, large subunit	2.1
	408805	H65912	Hs.48269	TM_pkinase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS_CUB_NTR_MAM_TIL_TILa_vwd,EP	procollagen C-endopeptidase enhance	2.1
10	447827	U73727	Hs.19718	SS_TM_Y_phosphatase_fn3_ig_MAM	protein tyrosine phosphatase, recep	2.1
	428273	A867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS_TM_pkinase_fn3	NM_002944 Homo sapiens v-ros avian	2.1
	403133			pkinase_K_Jeha_Band_41,RhoGEF	Target Exon	2.1
	440249	AJ246590	Hs.337275	VHL_TalD_DNase	ESTs	2.1
15	438580	AA811262	Hs.299202	TM_pkinase_sugar_Ir	ESTs	2.1
	406400			SS_TM_trypsin	NM_007198 Homo sapiens kallikrein 8	2.1
	427375	AL035460	Hs.177536	SS_Zn_carbOpept_pkinase5_Repro	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS_Granin_CDIP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
20	420757	X78592	Hs.99915	TM_hormone_rec_Androgen_recep,	androgen receptor (dihydrotestoster	2.1
	425018	BE245277	Hs.154195	DNase_J_K_tela	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM_E1-E2_ATPase_HydrodaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_Isomerase	ESTs	2.1
	407305	AA715284	Hs.38774	TM_pkinase_Sema_Plexin_repeat,	gb:mv35f03.r1 NCL_CGAP_Bx5 Homo sep	2.1
	456327	H68741	Hs.38774	TM_Glyco_Transf_B	ESTs	2.0
25	422429	A3A10527		pkinase_RGS_PH_pkinase_PH_RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRH_hormone5_hormone4	gonadotropin-releasing hormone 2	2.0
	45B016	AW188099	Hs.131813	pkinase	ESTs	2.0
	452194	AA694413	Hs.332849	TM_7m_3_ANF_receptpr_sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182038	TM_pkinase_MBD	Interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	pkinase_II_pxygenase_PLATipox	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM_DEAD_helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W800363	Hs.58446	pkinase_Furin-like_Recep_L_dom	ESTs	2.0
	418140	BE613836	Hs.83551	TM_E1-E2_ATPase	microfibril-associated protein 2	2.0
35	430076	AA465115	Hs.318773	AAA_BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.159448	Ribosomal_L7Ae_LRR_LRRCT_pkina	surfact 2	2.0
	425855	AF135025	Hs.159579	SS_trypsin	kallikrein 12	2.0
	400135	L40027	Hs.118890	pkinase	glycogen synthase kinase 3 alpha	2.0

40 TABLE 14B

Pkey: Unique Eos probasset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

45 Pkey CAT number Accessions

50	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
	418804	179138_1	AA809632 A917245 A1701732 AA228406
	420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
	422429	210469_1	A3A10527 AW962296 Z44865 H06641
	422689	219896_1	AW856665 AA315006 AW954733
	436399	405576_1	AA679463 AW813779 AW813709
55	438390	45662_1	AI422017 AI422946 AI363249 AI423113 A925592 A1420795 AI208187 AI423279 AI423545 A1424090 AI359637 A1D44732 D17003
	436993	457651_1	AA828995 AA834879 A926361
	452947	939810_1	AW130413 A9332362
	455092	1252971_1	BE152428 AW855572 AW855607
	457405	333127_1	AA504880 AA504911

60 TABLE 14C

Pkey: Unique number corresponding to an Eos probasset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	Nt_position
	400686	8118496	Plus	17982-18115,20297-20456
	401230	9929527	Minus	33835-34005,34539-34592,36461-36745,48925-49098,52804-52758
	401486	7341763	Plus	32585-32756,36291-36540,40791-40933,44018-44179
75	402337	6957691	Plus	4116-4288,16811-16973,17107-17258,19715-20040,22029-22205
	402481	9797406	Plus	87691-88891
	403133	7331427	Plus	38314-38634
	403471	9930659	Minus	88867-89583
	403763	7229888	Minus	43575-43887
80	404184	4581418	Minus	12652-13548
	404274	9885188	Plus	104127-104318
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 95th percentile value amongst cervical cancers was greater than or equal 80 units.

Pkey: Unique Eos probeID identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMRA1004341	36.2
	428227	AA321649	Hs.2248	small inducible cyclokinase subfamily B (Cys-X-Cys), mem	35.5
20	421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
	454390	AB202713	Hs.55956	KIAA0306 protein	30.5
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
	433226	AW503733	Hs.9414	KIAA1488 protein	30.0
25	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
	411689	BE812676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
	414132	AB01235	Hs.48480	ESTs	28.3
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
	448589	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
30	432906	BE265489	Hs.3123	lethal giant larvae (<i>Drosophila</i>) homolog 2	27.2
	418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldohyde red	26.9
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
	449722	BE280074	Hs.23960	cyclin B1	26.2
	414812	XZ2765	Hs.77357	monokine induced by gamma interferon	25.3
35	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
	432817	NM_014125	Hs.279812	PR00327 protein	24.6
	412630	AA768268	Hs.286273	hypothetical protein FLJ13346	23.6
	457465	AW301344	Hs.122908	DNA replication factor	23.1
	408808	AW867814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
40	428083	Y09397	Hs.227817	BCL2-related protein A1	22.9
	401405			Target Exon	22.8
	426272	AW450571	Hs.189284	ESTs	22.7
	424878	H57111	Hs.221132	ESTs	22.6
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinsin 6)	22.5
45	444371	BE540274	Hs.239	forkhead box M1	22.2
	418030	BE207573	Hs.83321	neuromedin B	22.0
	452291	AF015692	Hs.28853	CDC7 (cell division cycle 7, <i>S. cerevisiae</i> , homolog)-	21.6
	400198			Eos Control	21.3
50	416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
	424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
	438011	AB466173	Hs.145696	splicing factor (CC1.3)	20.7
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
	436923	AW293704	Hs.122658	ESTs	20.2
	415791	HO9366	Hs.76853	uracil-DNA glycosylase	20.0
55	448775	AB025237	Hs.398	nudix (nucleoside diphosphate linked moiety X)-type m	19.6
	435647	AI853240	Hs.49823	ESTs	19.6
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
	428486	AF165827	Hs.203963	hypothetical protein FLJ10339	19.5
	428433	AA521410	Hs.41371	ESTs	19.4
60	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
	417308	H60720	Hs.81692	KIAA0101 gene product	19.2
	429574	BE280321	Hs.208912	hypothetical protein MGC861	19.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
	408801	AK001330	Hs.46855	hypothetical protein FLJ10488	19.0
65	438899	AF085833	Hs.135624	ESTs	19.0
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
	438558	AB005943	Hs.326057	hypothetical protein MGC5178	18.8
	408908	BE286227	Hs.250822	serine/threonine kinase 15	18.8
	427488	M81401	Hs.178658	RAD23 (<i>S. cerevisiae</i>) homolog B	18.6
70	400195			MM_007057" Homo sapiens ZW10 Interactor (ZWINT), tran-	18.5
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosin)	18.4
	410324	AW282539	Hs.30177	ESTs	18.3
	453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
	410608	AI638438	Hs.159087	ESTs	18.1
75	432503	AA551196	Hs.188952	ESTs	17.9
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSmB	17.7
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
	449962	AA004879	Hs.187620	ESTs	17.3
	425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
	440774	AI420511	Hs.127832	ESTs	16.8
80	408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [16.7
	426897	AW976570	Hs.97387	ESTs	16.5
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

			kinasin-like protein 2	16.3	
	433159	AB035898	Hs.150587	polymerase (DNA directed), theta	16.3
	430465	AF052573	Hs.241517	cofactor required for Sp1 transcriptional activation,	16.3
	453883	A1538516	Hs.22630	Bloom syndrome	16.1
	453941	U39817	Hs.36820	phosphoserine aminotransferase	16.0
5	438461	AW075485	Hs.295049	ESTs, Weakly similar to Y228_HUMAN HYPOTHETICAL PROTEIN	16.0
	407999	AH126271	Hs.49433	Homo sapiens cDNA FLJ12981 fts, clone NT2RP2006454	15.7
	413943	AW294416	Hs.144687	KIAA1355 protein	15.6
	407720	AB037776	Hs.38002	ESTs, Moderately similar to Y14342 NSD1 protein - mouse	15.6
	425318	AA354977	Hs.191655	matrix metalloproteinase 12 (macrophage elastase)	15.5
10	423573	BE003054	Hs.1695	ESTs	15.3
	419777	DG0134	Hs.270975	ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor	15.2
	453986	R66282	Hs.20247	cyclin E1	15.2
	443715	A153187	Hs.9700	telraspan 1	15.2
	407786	AA587538	Hs.38972	hypothetical protein FLJ23045	15.2
15	431910	AK000142	Hs.101774	glutathione synthetase	15.1
	417634	W27202	Hs.82327	ESTs	15.1
	432892	AW974944	Hs.200577	small inducible cytokine subfamily A (Cys-Dys), member 1	15.1
	446921	AB012113	Hs.16530	ubiquitin fusion degradation 1-like	15.0
20	427999	A1435128	Hs.181369	interleukin 2 receptor, beta	15.0
	413869	NM_000878	Hs.75596	Interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	431629	AU077025	Hs.265827	ESTs	14.8
	435354	AAG78267	Hs.117115	immunoglobulin kappa constant	14.8
	406836	AW514601	Hs.156110	suppressor of K transport defect 1	14.8
	416109	AJ420311	Hs.126650	thymidylate synthetase	14.7
25	417933	X02308	Hs.82952	ESTs	14.7
	438970	AA837782	Hs.321058	ESTs	14.7
	409580	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
30	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420734	AW972672	Hs.293736	ESTs	14.5
	434266	AJ378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960573	Hs.177530	ATP synthase, H transporting, mitochondrial F1 complex	14.3
35	427081	AH474533	Hs.170528	ESTs, Moderately similar to ALU_C_HUMAN III ALU CLASS	14.2
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU_S_HUMAN ALU SUBFAMILY SC S	14.2
	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391884	Hs.62861	guanylate binding protein 1, Interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
40	418803	U50079	Hs.88556	histone deacetylase 1	14.0
	434094	AA305999	Hs.238205	hypothetical protein PRO2013	14.0
	420139	NM_005367	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding protein	13.9
	433255	AJ274270	Hs.96840	KIAA1527 protein	13.9
45	431838	AJ097229	Hs.217484	ESTs, Weekly similar to ALU_I_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.268900	hypothetical protein FLJ23231	13.8
	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
50	404630			Target Exon	13.6
	408321	AW405882	Hs.44205	corin	13.6
	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE663085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219*_gi 12737260 ref XP_006682.2 keratin 18 [Homo sapiens]	13.5
55	456614	AV663110	Hs.108650	hypothetical protein FLJ20539	13.5
	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
	439926	AW014875	Hs.137007	ESTs	13.3
	411263	BE297902	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin)	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
60	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109280A B cell growth factor	13.2
	410668	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
65	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.1
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated protein)	13.0
	413314	BE081565	Hs.15685	gi QV2-BT0835-210400-156-b07 BT0835 Homo sapiens cDNA	13.0
	430929	AA489165	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200286	ESTs	12.9
70	400298	AA032278	Hs.81635	sarcolemma membrane epithelial antigen of the prostate	12.8
	417105	X60982	Hs.81226	CD6 antigen	12.6
	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferritin associate	12.6
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
75	437056	AI147061	Hs.16954	gi X0k3Ja11.s1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens	12.5
	438768	AI307418	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AAD10907	Hs.184458	hypothetical protein	12.4
	418205	L21715	Hs.83760	tropomodulin I, skeletal, fast	12.4
	442994	AI026718	Hs.16954	ESTs	12.4
80	433301	AW295280	Hs.152016	Homo sapiens cDNA: FLJ22140 fts, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S85657 alpha-1C-adrenergic receptor	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-) glycoprotein beta-1,4-N-acetylgalactosaminidase	12.3
	422765	AW408701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
	432325	AW973209	Hs.261782	ESTs	12.3
5	414761	AU077228	Hs.77256	enhancer of zeste [Drosophila] homolog 2	12.3
	418618	U86097	Hs.85724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
	416443	T07353	Hs.7948	ESTs	12.1
	429770	AT766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
15	432810	AA863400	Hs.23054	ESTs	12.1
	434423	NM_006769	Hs.3844	UM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW808906	Hs.334787	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002565	11.9
	407804	AF228603	Hs.39857	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
	434408	A031771	Hs.132586	ESTs	11.8
	406747	A1925153	Hs.217493	annexin A2	11.8
25	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_00235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445865	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427527	A080957	Hs.302063	immunoglobulin heavy constant mu	11.7
	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10196 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.58009	2'-S'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
	409331	BE203233	Hs.129771	ESTs	11.4
35	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3/hnRNP methyltr	11.4
	456880	AW015844	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
	433849	BE465884	Hs.280728	ESTs	11.4
40	430519	AF129534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	A1905780	Hs.198272	Target CAT	11.3
	422713	AA302780	Hs.119326	Huntingtin-interacting protein A	11.3
	443491	AW499865	Hs.9456	SWNSNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	A1686945	Hs.272062	ESTs	11.2
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 5730578N08 gene,	11.2
	442737	AB002319	Hs.8663	KIAA0321 protein	11.2
50	409113	AA074887		gb:zn18z05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30809	KIAA0430 gene product	11.0
55	436777	AW503116	Hs.301818	zinc finger protein 146	11.0
	414706	AW340125	Hs.76089	KIAA0197 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J 6E	11.0
	438895	A1277996	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gb:cn176g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	HB5689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AA393122	Hs.134726	ESTs	10.9
	444655	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
	410093	AW569558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
65	400080			Eos Control	10.8
	424517	AA539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675: Homo sapiens promyelocytic leukemia (PML),	10.8
	448099	T93096	Hs.17125	hypothetical protein MGC15912	10.7
	451056	A766650	Hs.206132	ESTs	10.7
70	408235	AA188927	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AA486888	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
75	438854	AI005270	Hs.123543	ESTs	10.6
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AI815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AI056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	10.5
	430975	AW326081	Hs.6817	Inosine triphosphatase (nucleoside triphosphate pyroph	10.6
80	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812635		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC 8	10.5

416584	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fts, clone MAMMA1001501, h	10.5	
447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fts, clone NT2RM4002390	10.5	
408329	AF165510	Hs.44227	heparanase	10.5	
5	410146	AW592655	gb:hf45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5	
427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2{	10.4	
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4	
407241	M34516		gb:Human omega light chain protein 14.1 (lg lambda ch	10.4	
435061	AI651474	Hs.163944	ESTs	10.4	
409653	AW7451693	Hs.220826	ESTs	10.4	
10	428294	AA425488	gb:zw46d02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiie	10.4	
433160	AW207002	Hs.134342	TASP for taste-specific adriamycin sensitivity prote	10.4	
408809	AW274873	Hs.279708	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4	
410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4	
15	424792	U92538	origin recognition complex, subunit 5 (yeast homolog)	10.3	
422406	AF025441	Hs.116208	Opa-interacting protein 5	10.3	
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelat	10.3	
413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymph	10.3	
413507	BE145360	Hs.190084	ESTs, Weakly similar to I38022 hypothetical protein [10.3	
20	448119	H38587	dedicator of cyto-kinase 1	10.2	
457288	AA521458	Hs.192738	ESTs	10.2	
402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2	
440572	AW183778	Hs.249504	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2	
453323	AF034102	Hs.32851	solute carrier family 2B (nucleoside transporters), m	10.2	
25	443780	NM_012068	activating transcription factor 5	10.1	
422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1	
444314	A1140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1	
426125	X67241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1	
430848	AW021726		gb:dt27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1	
30	422470	A017919	peptidyl arginine deiminase, type V	10.1	
449501	A1652924	Hs.231942	ESTs	10.1	
420731	AL042082	Hs.104432	ESTs	10.1	
404345	AAT30407	Hs.159155	protocadherin 11	10.1	
400438	AF185611		Target	10.1	
35	438170	A1918685	ESTs	10.1	
432193	AA372254	Hs.273193	hypothetical protein FLJ10706	10.1	
458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1	
427766	AA412258	Hs.188817	ESTs	10.1	
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0	
403038			Target Exon	10.0	
40	434674	AAB31879	ESTs	10.0	
439885	AW956781	Hs.283937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0	
439428	AA835825	Hs.190490	ESTs	10.0	
403310			Target Exon	9.9	
45	408392	U28831	Hs.44586	9.9	
421849	AW410872	Hs.108894	KIAA1641 protein	9.9	
433384	A1021992	Hs.124244	hypothetical protein FLJ20411	9.9	
443343	BE409809	Hs.301006	ESTs	9.9	
437287	AW511443	Hs.258110	purine-rich element binding protein B	9.9	
455978	A1310161	Hs.173524	ESTs	9.9	
50	435851	AAT00946	ESTs	9.9	
452243	AL355715	Hs.286555	programmed cell death 9	9.8	
441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.8	
414001	A1610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.8	
55	436869	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
421602	AF111856	Hs.106039	solute carrier family 34 (sodium phosphate), member 2	9.8	
417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fts, clone HEMBA1001835	9.8	
455855	BE147440		gb:RC1-HT0229-080100-016-f09 HT0229 Homo sapiens cDNA	9.8	
410390	AA876305	Hs.125286	ESTs	9.8	
60	418626	BE019020	solute carrier family 16 (monocarboxylic acid transpo	9.8	
442660	AW138174	Hs.130851	ESTs	9.8	
436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8	
428773	NM_015556	Hs.172180	KIAA0440 protein	9.8	
.65	413476	U25849	acid phosphatase 1, soluble	9.7	
416347	AA216419	Hs.5212	gb:nc18e03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone s1	9.7	
448752	AA593857	Hs.300842	KIAA1608 protein	9.7	
440349	AA684196	Hs.31476	Homo sapiens cDNA FLJ13872 fts, clone THYRO1001322	9.7	
431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7	
430752	AA485330	Hs.303278	ESTs	9.7	
70	436523	BE612890	single-strand selective monofunctional uracil DNA gly	9.7	
415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7	
411930	FO8485	Hs.7740	oxysterol binding protein-like 1	9.7	
430392	AI073913	Hs.100688	ESTs, Weakly similar to JE0350 Anterior gradient-2 (H	9.7	
452234	AW084176	Hs.223236	ESTs, Weakly similar to I38022 hypothetical protein [9.6	
409997	A1908055	Hs.57749	synaptic nucleol expressed gene 2; KIAA1011 protein	9.6	
75	434957	AF283775	x001 protein	9.6	
407292	AA876638	Hs.35380	gb:nc45e08.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone s	9.6	
459109	AW292447	Hs.140821	ESTs	9.6	
457892	AA744389		gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sapiens cDNA clone s	9.6	
80	432074	AA525248	ESTs	9.6	
440463	A1733087	Hs.129994	ESTs	9.6	
420851	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6	
445326	AI220072	Hs.165893	ESTs	9.6	
434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALIN [Hsap	9.6	

	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123664	ESTs	9.6
5	417037	BE083936	Hs.30976	antigen identified by monoclonal antibody Ki-57	9.6
	449317	AV293413	Hs.132906	19A24 protein	9.6
	435588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374 ^a ;gi 10764778[gb]AAG22817.1 AF302150_1 (AF30	9.5
10	414065	AW516373	Hs.271249	Homo sapiens cDNA FLJ13580 fs, clone PLACE1008851	9.5
	409902	AI337658	Hs.156351	ESTs	9.5
	432258	AV973078	Hs.293039	ESTs	9.5
	438581	AV977766	Hs.292133	ESTs, Moderately similar to I78886 serine/threonine-s	9.5
	405536			NM_005805;Homo sapiens 26S proteasome-associated pad1	9.5
15	418216	AA662240	Hs.283099	AF15q14 protein	9.5
	434573	AV372340	Hs.159717	ESTs	9.5
	439354	AF086174		gb:Hom sapiens full length insert cDNA clone Z994A08	9.5
	455410	AV936578		gb:PM2-DT0023-080300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400738			Target Exon	9.5
	419474	AV966819	Hs.155849	ESTs	9.4
	406464			C17000168 ^a ;gi 7294725[gb]AAF50062.1 (AE003644) CG7547	9.4
	407881	AV072003	Hs.40988	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400081	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
25	433B40	AA129782	Hs.3678	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423842	AV452650	Hs.157148	hypothetical protein MGC13204	9.4
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
30	419988	W39388	Hs.55338	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441076	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
35	420897	AV139261	Hs.232280	ESTs	9.3
	418857	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI198510	Hs.267912	ESTs, Weakly similar to ALU_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T79799	Hs.18214	ESTs, Weakly similar to B34067 hypothetical protein [9.3
40	420101	AV500529	Hs.93180	KIAA0767 protein	9.3
	428168	AA423849	Hs.79530	MS-14 protein	9.3
	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92562	Hs.36052	ESTs	9.3
	454765	AV819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
45	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA, partial cds	9.3
	416505	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
	416509	C75253	Hs.220950	ESTs	9.3
	429845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.126376	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase	9.2
	417881	AI879117		gb:cau54g09.y1 Schmidler fetal brain 00004 Homo sapien.	9.2
50	446354	AV449650	Hs.202249	ESTs	9.2
	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22283 fs, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459306	Hs.24908	ESTs	9.2
55	457322	AB154686	Hs.243901	Homo sapiens cDNA FLJ20738 fs, clone HEP08257	9.2
	424317	AI885032	Hs.26017	ESTs	9.2
	433001	AF217513	Hs.279805	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
60	434980	AV374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	tRNA selenocysteine associated protein	9.1
	439158	R63023	Hs.193688	ESTs	9.1
	443081	HE6858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
65	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFEIT LOCUS	9.1
	437044	AI035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
	430780	N95102	Hs.334658	hypothetical protein MGC12250	9.1
	426793	X89867	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	A4218940	Hs.137516	fidgetin-like 1	9.1
70	431405	AI470895	Hs.252574	ribosomal protein L10a	9.0
	405454			C12000541;gi 57298B4 ref NP_006539.1 IGF-II mRNA-bl	9.0
	438362	AA805578	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT2RP2003117	9.0
75	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
	418653	A1734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437834	A4814471	Hs.291800	ESTs	9.0
80	435074	AT680944	Hs.116937	ESTs	9.0
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699985	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AAB14971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
5	437965	AW891130	Hs.38173	ESTs	8.9
	426360	AW290881	Hs.211295	ESTs, Weakly similar to 2108260 B cell growth factor	8.8
	448111	AA053486	Hs.20315	interferon-induced protein with tetrabasic peptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
	429228	A1553633	Hs.337139	ESTs	8.8
10	433914	AF108138	Hs.12160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length Insert cDNA clone EUROI	8.8
	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
15	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	A1146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
20	408805	H58912	Hs.48269	vaccinia related kinase 1	8.7
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	449148	NM_0016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
	454132	AW131759	Hs.245286	ESTs	8.7
25	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.78078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241867	Hs.127728	ESTs	8.7
	459539	A1279186	gb cpm24a04.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone 3'		8.7
30	443148	A1034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
	424255	A1192657	Hs.143897	dysterin, limb girdle muscular dystrophy 2B (autosome	8.7
	459495	AA320038	Hs.120292	gb EST22383 Adipose tissue, white II Homo sapiens cDN	8.7
	443117	A1248826	Hs.42029	ESTs	8.6
	457434	AW628192	Hs.18B51	hypothetical protein FLJ10875	8.6
	442505	AV030775	Hs.198248	UDP-GalbetaGalNAc beta 1,4-galactosyltransferase, p	8.6
35	430901	AA488833	Hs.126711	ESTs, Weakly similar to t38588 reverse transcriptase	8.6
	438223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995	Hs.155919	gb HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
	415961	H10983	Hs.155919	ESTs	8.6
40	424042	Y10501	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
	451035	AU076765	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100605	Hs.1216557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA458195	Hs.10056	hypothetical protein FLJ14621	8.6
	458042	AW058464	Hs.6430	protein with polyglutamine repeat; calcium (ca2) home	8.6
45	456530	AI049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp58B1E1120 (from clone DKF	8.6
	433345	A1681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445008	W91903	Hs.124814	ESTs	8.6
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900	Hs.1216557	gb MRU-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
50	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae}	8.5
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	416018	U49395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C11001758^;gb 12621132 ref NP_075243.1 MEGF1 Rattus	8.5
55	438451	AI081972	Hs.220261	ESTs	8.5
	435176	AA744875	Hs.189413	ESTs	8.5
	443246	AI040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subunit	8.5
	403899			Target Exon	8.5
60	434932	BE613162	Hs.284135	hypothetical protein MGC3036	8.5
	420991	AW504014	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE6547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE173190	Hs.173190	gb RCO-HT0813-210300-032-07 HT0813 Homo sapiens cDNA	8.4
	402798			Target Exon	8.4
65	423426	AW389579	Hs.128434	Homo sapiens ELJSC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp584D0472 (from clone DKF	8.4
	404110			NM_020245^;Homo sapiens tubby super-family protein (T	8.4
	424441	X14850	Hs.147097	H2A histone family, member X	8.4
	431155	AL037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
70	414839	X33692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	8.4
	406087	AA157857	Hs.182265	keratin 19	8.4
	418278	AI088489	Hs.83937	hypothetical protein	8.4
	458696	AW375333	Hs.199890	ESTs	8.4
	456248	AL035788	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
75	403152	AA576664	Hs.37078	v-crk avian sarcoma virus C110 oncogene homolog-like	8.4
	407649	BE0665724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19k24 protein	8.4
	425891	AI041717	Hs.132141	ESTs	8.4
80	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapien	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587	Hs.182625	gb JL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	426144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4